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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      Minimum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein -
                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                         Title:
                                                                                                                                                number of hits satisfying chosen parameters:
                                                                                    seq length: 0 seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                            July 26, 2000, 13:15:21 ; Search time 33.21 Seconds (without alignments) 99.138 Million cell updates/sec
                                                                                                                                                                                         188963 seqs, 23686106 residues
                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                         US-09-203-768A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                MKHLWFFLLLVAAPRWVLSQ.....ARPHRYFDYWGQGTLVTVSS 139
                                                                                                                                                    188963
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

A\_Geneseq\_36:\*

## SUMMARIES

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		,			SUMMARTES	
Result	Score	Query Match	Length	DB	ID	Description
<u>.</u>	N 1	83.2	116	ᆸ	R66324	Human immunoglobul
N	575.5	76.9	472	$\vdash$	R93166	-rhesus I
w	•	74.9	136	Н	W24536	lin
4	58.		123	Н	W03757	
v	58.	•	142	ب	R41285	nge
თ	S	73.8	128	H	R12269	
7	IJ	•	116	۳	R42689	Vh 71-4. DNA segme
8	55	•	116	Н	R66346	Human immunoglobul
9	٠	•	476	<b>,</b>	W01822	Primatised anti-hu
10	41.	72.4	476	بر	W63765	Macaque primatized
11	ω	72.1	118	μ	R66348	Human immunoglobul
12	ω	٠	475	μ	R93553	Monoclonal antibod
13	53	71.9	116	_	R66298	Human immunoglobul
14	36.	71.7	140	-	W32477	Anti-CD4 cynomolgu
15	٠	71.7	140	_	W43430	Monkey anti-CD4 he
16	30	71.7	141	۳	R31948	Anti-CD4 VH peptid
1/	36.	/1./	46/	-	W14927	Human gamma-4PE ne
18	36.	71.7	467	-	W14925	Human gamma-4 heav
19	36.	71.7	467	ш	W14926	1-4E h
20	53	•	141	ш	W70378	Anti-human CD23 6G
21	32.	•	139	μ	W14922	Monkey anti-CD4 he
22	32.	•	139	μ	W35284	Monkey anti-human
23	32.	•	139	ب	W53988	4
24	30.	٠	134	μ	4	P.
25	30.	•	134	<b>-</b>	N	-
26	30.	•	134	-	œ	۳
27	29.	٠	121	Н	_	Anti-human RhD FOM
28	•		476	_		Primatised anti-hu
29	29.	٠	476	,	ത	Macaque primatized
30	N		118	Н	N	nunoglobu
i u	) () ()	70.5	125	٠,	P81259	Variable region of
	٠.	٠	1139	۰ -		Anti-CD4 antibody
33	Ń	69./	RTT	-	R66322	Human immunogiobul

Query Match Best Local 9 Matches

Length 116;

## ALIGNMENTS

HACE BERROTTER TO SOLUTION OF THE SOLUTION OF O78917-38. The genes are subdivided into 5 families of vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with Tag1 restriction enzyme. The fragments were separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with Cla1-digested cosmid vector pJB81. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts. immunoglobulin in mammalian Sequence 116 AA; DNA fragment comprising human immunoglobulin vh genes - for the production of human immunoglobulin in mammalian hosts Claim 41; Page 74-75; 130pp; Japanese.
Protein sequences (R66295-51) are novel human immunoglobulin heavy chain protein sequences isolated genes. The genes (Q78939-79002) were isolated and cloned from a series of cosmid constructs Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR amplification using primers 24-NOV-1994; 10-MAY-1993; 10-MAY-1993; Human immunoglobulin variable heavy chain #30. Primer; PCR; amplify; human; immunoglobulin; v cosmid; placenta; vector; pJB81; E.coli; mamma (NISB ) JAPAN TOBACCO INC Honjo T, Matsuda F; WPI: 95-006791/01. 03-AUG-1995 • (first entry) R66324 standard; Protein; 116 A variable; heavy chain;

RESULT
R93166
R9
AC
R9
DT 3C
DE An 밁 밁 Š Ş 30-OCT-1996 (first entry)
Anti-rhesus D recombinant antibody D7C2 heavy chain. R93166 standard; Protein; 472 R93166; 30-OCT-1996 (first entry) 61 61 GKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 116 1 MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP 60 1 MKHIMFFILLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP 60 GKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 116 al Similarity 116; Conserva Conservative 83.2%; Score 622; DB 1; 1 100.0%; Pred. No. 3.8e-45; tive 0; Mismatches 0; A A Indels 0; Gaps

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W24536
ID W2
AC W2
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Best Local S
Matches 115
  protein
J09140386-A.
03-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haemolysis in new-born babies

Example 2; Page 35-37; 46pp; French.

The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive babies.

Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of a recombinant IgM-D7C2 heavy chain fused downstream of a mouse VH signal peptide. Sequence 472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human monoclonal a rhesus positive; pariable region; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T26889.
Recombinant anti-rhesus D monoclonal baculovirus-transformed insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-1996.
02-SEP-1994; 010566.
02-SEP-1994; FR-0105
                                                                                                                                                                                                    09-CCT-1997 (first entry)
Immunoglobulin rB6B7 heavy chain variable region.
Immunoglobulin; variable region; heavy chain; thyrot;
thyroid stimulating activity; light chain; Basedow's
                                                                                                                                                                                                                                                                                                              W24536;
                                                                                                                                                                                                                                                                                                                                W24536 standard;
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WPI; 96-162018/17.
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(PROT-) PROTEINE PERFORMANCE.
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                                                                                                                                                     sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDPWGQGTTVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
115; Conserv
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                                                      /note= "signal peptide"
20. .136
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rhesus negative; haemolysis; gamma 1 heavy chain;
insect host cell; baculovirus; recombinant production.
                                                                                                                                                                                                                                                                                                                                   Protein; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- signal_peptide
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human gamma 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 575.5; DB:
Pred. No. 1.1e-40;
3; Mismatches 1:
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m anti-rhesus D
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                                                                                                                                                                                                                                thyrotropin receptor;
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                                                                                                                                                                                                         disease;
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Best Local Sin
Matches 111;
                                                                                                                08-MAR-1996.
02-SEP-1994; 010566.
02-SEP-1994; FR-010566.
02-SEP-1994; FR-010566.
(INSP ) INST PASTEUR.
(PROT-) PROTEINE PERFORMANCE.
Chaabihi H, Edelman L, Kaczol
WPI; 96-162018/17.
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22-NOV-1995; JP-328
(EIKE) EIKEN KAGAK
WPI; 97-344899/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thyroid function stimulating activity

Claim 31; Page 14-15; 18pp; Japanese.

W24536-W24539 represent the immunoglobulin heavy and light chain variable regions isolated from peripheral blood lymphocyte strains. These sequences were isolated from the B6B7 and 101-2 strains of peripheral blood lymphocytes of a Basedow's disease patient. These sequences are replaced, deleted or inserted into an antibody, to create the antibodies of the invention. The antibodies of the invention have thyroid function stimulating activity, and act by combining with thyrotropin receptor. The antibody can be used in a method to detect autoantibodies which have thyroid function stimulating activity.

Sequence 136 AA;
haemolysis in new-born bables
Example 1; Page 32; 46pp; French.
The human monoclonal antibody D7C2, of isotype IgM, recognises a
30-32 kD polypeptide on the membrane of rhesus positive red blood
cells. The antibody agglutinates rhesus positive cells but not
                                                                                                                                                                                                                                                                                                          region
                                                                                                                                                                                                                                                                                                                                                                                                                                                       W03757 standard; Protein; 123 AA. W03757; 29-OCT-1996 (first entry)
                                                                         Recombinant anti-rhesus D monoclonal baculovirus-transformed insect cells
                                                                                                       N-PSDB; T26870
                                                                                                                                                                                                                                                                                                                                                                                              Anti-rhesus D monoclonal antibody D7C2 heavy chain v region. Human monoclonal antibody; immunoglobulin isotype IgM; aggit rimesus positive; rhesus negative; haemolysis; heavy chain; variable region; insect host cell; baculovirus; recombinant
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                                                                                                                                                                                                                                                                 region
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                                                                                                                                    Kaczorek M,
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Pred. No. 5.7e-40;
4; Mismatches 18
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RESULT
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                                                             Matches
                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                     and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection
Claim 9-10; Page 77; 109pp; English.
mRNA from the known hybridoma F105 was converted to CDNA and this subjected to PCR amplification using primers corresp. to appropriate parts of the heavy or light chains and having restriction sites to permit cloning. The extension prods. were isolated and sequenced. The recombinant human monoclonal antibody (MAb) binds to a discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks the binding of gp120 to the CD4 receptor, and neutralises a broad deficiency, esp. at doses of 0.1-10 mg/kg.

Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive bables. Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of the variable region of the IgM-D7C2 heavy chain.
                                                                                                                                                                                                                                                                                                                                                        Haseltine WA, Marasco WA,
WPI; 93-214174/26.
N-PSDB; Q49154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F105 rearranged variable region heavy chain.
Monoclonal antibody; MAD; envelope; glycoprotein; gpl20; HIV; AIDS;
CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
chain; epitope; immune deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1992; U10928.
10-DEC-1991; US-804652.
(DAND ) DANA FARBER CANCER INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9312232-A.
24-JUN-1993.
                                                                                                                                                                                                                                                                                                                                          DNA segments encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R41285 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 VSS 139
                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN 79
MKHLWEFILLIVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSLKSRVTISVDTSKNQFSLKLNSVTAADTAVYYCARAPEYKWKYHGDWFDPWGQGTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR--EIAARPH-RYFDYWGQGTLVT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLQQWGAGLLKPSETLSLTCTVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= sig_peptide
20. .142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ybridoma; polymerase immune deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.7%;
                                                                           74.78;
                                                                                                                                                                                                                                                                                                                          g monoclonal antibody -
for treating AIDS, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_protein
                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                         Posner MR,
                                                                           Score 558.5; DB 1
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 558.5;
Pred. No. 7.
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                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; DB 1;
7.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                         Sodrosk1
                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                          which binds to for diagnosing
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                                                                                          Length
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                                                             Indels
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                                                                                           142;
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                                                                                                                                                                                                                                                                                                                           gp120
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RESULT R42689

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R42689 standard; Protein; 116 AA. R42689; 01-NOV-1993 (first entry) Vh 71\*4

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                                                                                                                                                   Query Match
Best Local
                                                                                                                                         Matches
                                                                                                                                                                                                                     DNA encoding complementary determining regions - of human anti-rhesus D antibodies, useful in prodn. of monoclonal antibodies and for passive immunisation

Placiosure; Fig 8; 32pp; English.

The DNA sequence of eleven monoclonal antibodies are represented in 0119145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols. having varied binding specificity. The chimaeric anti-RhD antibodies can be used for diagnosis and therapy, and are capable of providing blood-typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the newborn.
                                                                                                                                                                                                                                                                                                                                                                                                                    WO9107492-A.
30-MAY-1991.
13-NOV-1990;
13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                               13-NOV-1990; E01964.
13-NOV-1989; GB-025590.
(BLOO-) CENT BLOOD LAB AUTH.
Hughes- Jones N;
WPI; 91-178104/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R12269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-1991 (first entry)
Anti-human RhD FOM-1 MAB (VH chain).
Monoclonal antibody; rhesus D; blood-typing;
haemolytic disease of the newborn; HDN
                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q11951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
120
                                                                                                                                                                                                                newborn
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                                                                                         QGTLVTVSS 139
                                            PSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARGL-ERPIRNQLLNRLGYYMDVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPHRYFDY----WGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGTTVTVSS 128
                                                                    PSLKSRYTISVDTSKNQFSLKLSSYTAADTAVYYCAREIAARPHR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVF-YGDYRLDPWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                    Similarity
                                                                                                                                                                                                    128 AA;
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- CDR2
98. .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR1
50. .65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 31. .35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                   73.8%;
                                                                                                                                       Score 552; DB 1;
Pred. No. 2.7e-39;
4; Mismatches 7
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                                                                                                                                                                Length 128;
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                                                                    -YEDYWG 130
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Best Local
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                                                                                             10-MAY-1993; J00603.
10-MAY-1993; WO-J00603.
(NISB ) JAPAN TOBACCO INC.
HODJO T, MATSUDA F;
WPI; 95-006791/01.
N-PSDB; Q78997.
   DNA fragment comprising human immunoglobulin Vh genes - for the production of human fragment in nammalian hosts production of human framunoglobulin in mammalian hosts production of human framunoglobulin production sequences (R66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (Q78939-79002) were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;
                                                                                                                                                                                                                                  04-AuG-1995 (first entry)
Human immunoglobulin variable heavy chain #52.
Primer; PCR; amplify; human; immunoglobulin; variab
cosmid; placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA segments encoding monoclonal antibody - which binds to gp120 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection monitoring HIV infection Disclosure; Page 64; 109pp; English. The monoclonal antibodies (Ab26 - Q42702) and 268-D - Q42703), which by nucleotide sequence analysis, appear to use a rearranged which by nucleotide sequence analysis, appear to use a rearranged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS; CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light; chain; epitope; immune deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haseltine WA, Mar
WPI; 93-214174/26.
N-PSDB; Q42697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                         Homo sapiens.
W09426895-A.
                                                                                                                                                                                                                                                                                  R66346;
04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      many antigens.
Vh 71-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represents a naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vh 71-4 gene (Q42697). Ab26 (Q42702) was derived from CD5+ B cells of a healthy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-1992; U10928.
10-DEC-1991; US-804652.
(DAND ) DANA FARBER CANCER INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSDITAL
                                                                                                                                                                                         24-NOV-1994.
                                                                                                                                                                                                                                                                                                              R66346 standard; Protein; 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKHLWEFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSVSSYYWSWIRQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aturally occurring polyreactive antibody which binds to Ab26 shares greatest sequence similarity with germline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
69. .84
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20. .116
/label= mat_protein
49. .54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.5%;
90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 550; DB 1;
Pred. No. 3.6e-39;
3; Mismatches 8
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                                                                                                                                                                                                                                                  variable; heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                   chain;
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MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFS-GYYWSWIRQP 59

Query Match Best Local S Matches 108

Similarity

72.48; 74.08;

Score 541.5; DB 1 Pred. No. 7.7e-38; Mismatches

Length Indels

476; 7;

Conservative

11,

20; ۲.

Gaps

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Monkey monoclonal antibody binding human B7.1 or B7.2 antigen
Juseful for treating autoimmune disease or graft-versus-host disease
Claim 14; Fig 10B; B1p; English.
Claim 14; Fig 10B; B1p; English.
Claim 16; Fig 10B; Fig 15; Fig 15; Fig 15; Fig 16; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.9
Best Local Simplarity 90.9
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y6;Y24; 3-31; M84; M18 and M131, by PCR amplification using primers (778917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TagI restriction enzyme. The fragments were separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pJB81. The ligation products were in vitro packed and infected into 5.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human in mammalian hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W01822 standard; Protein; 476 AA.
W01822;
25-MAY-1997 (first entry)
Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
Monoclonal antibody; cynomolyus monke; macaque; 16C10;
primatised antibody; B7 antigen; CD28; immunosuppressive;
autoimmune disease; idiopathic thrombocytopaenia purpura;
systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
type 1 diabetes mellitus; graft versus host disease;
hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1996; U10053.
07-JUN-1995; US-487550.
(IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T62513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 97-108638/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09640878-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSVSSYYWSWIRQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brams P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 550; DB
; Pred. No. 3.6e
3; Mismatches
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No. 3.
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.6e-39;
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Best Local S
Matches 108
                                                                                                                                                                                                                                                                                                                                                    Idiopathic thrombocytopaenia purpura, systemic lupus crythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (II-2), T cell proliferation and antigen-specific immunoglobulin G (IGG) responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1998 (first entry)
Macaque primatized 16C10 heavy chain protein.
Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; II-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells, e.g. graft rejection or tumours

Example 7; Fig 5b; 87pp; English.

This sequence represents a primatized form of the antibody 16C10 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IDEC-) IDEC PHARM CORP
Anderson DR, Brams P, Ha
WPI; 98-286601/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1998.
29-OCT-1997; U19906.
08-NOV-1996; US-746361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h cell proliferation.
Macaca fascicularis.
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121
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LFSVVGMVYNNWFDVWGPGVLVTVSS
                                                                                                               PGKGLEWIGEI-NHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARE- 117
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                                     ---- IAARPHRYFDYWGOGTLVTVSS 139
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Pred. No. 7.7e-38;
1; Mismatches 20;
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Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA fragment comprising human immunoglobulin vh genes - for the production of human immunoglobulin in mammalian hosts Disclosure; Page 110-11; 130pp; Japanese.

Protein sequences (R66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (Q78939-79002) were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR amplification using primers Q78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta: The DNA was partially digested with Tag1 restriction enzyme. The fragments were separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pJB81. The ligation
                                                                                J08038178-A.
13-FEB-1996.
20-FEB-1995;
18-FEB-1994;
                                                                                                                                                                                                                                          20-AUG-1996 (first entry)
20-AUG-1996 (first entry)
MonocLonal antibody DNA heavy chain against 65 kD hcmv antigen.
Polymerase chain reaction; primer; amplify; PCR; light chain; PCP Polymerase chain reaction; primer; hcmv; heavy chain; diagno
                                                                                                                                                                                                                                                                                                                  R93553
R93553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunoglobulin variable heavy chain #54.
Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain; cosmid; placenta; vector; pJB81; E.coli; mammalian.
Human monpolonal antibody binds to cytomegalovirus
                 (NISN ) NISSHINBO IND
(TANA/) TANAKA H.
WPI; 96-154852/16.
N-PSDB; T18059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            products were in vitro packed and infected into E.coli 490A. The value of the subcloned by colony hybridisation. The value of the DNA fragments encoding them are useful in producing human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; Q78999.
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Honjo T, Matsuda F;
WPI; 95-006791/01.
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                                                                                                                                                                  protein
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Sequence 118 AA;
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10-MAY-1993; WO-J00603.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSVSSGSYYWSWIRQ
                                                                                                                                                                                                                                                                                                                                 standard;
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JP-021628
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20. .475
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89.0%;
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Pred. No. 3e-38;
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RESULT 13
R66298
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                                                                         Query Match
Best Local Similarity
Matches 103; Conser
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-1993; J00603.
10-MAY-1993; WO-J00603.
(NISB) JAPAN TOBACCO INC.
Honjo T, Matsuda F;
WPI; 95-006791/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in R93553-54 represent the heavy and light chains respectively of a monoclonal antibody against a 65 kb antigen of human cytomegalovirus (hCMV). The DNA's encoding these sequences were amplified using the sequences given in T18040-58. The monoclonal antibody may be used in the diagnosis of hCMV.
                                                                                                                                                                                                                                                       DNA fragment comprising human immunoglobulin vh genes - for the production of human immunoglobulin in mammalian hosts production of human immunoglobulin in mammalian hosts pisclosure; Page 34-35; 130pp; Japanese.

Protein sequences (R66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (Q78939-79002) were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR amplification using primers Q78917-38. The genes are subdivided into 5 families of vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TaqI restriction enzyme. The fragments were separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pUB81. The ligation
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Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain; cosmid; placenta; vector; pJB81; E.coli; mammalian.
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                                                                                                                                                                                     products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.
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                                   MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP 60
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AA;
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Pred. No. 1.2e-37;
6; Mismatches 18
                                                                         Score 538; DB 1;
Pred. No. 3.5e-38;
3; Mismatches 10;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new chimetic antibody (Ab) has been developed comprising a human or chimpanzee immunoglobulin (Ig) constant region and an Old world monkey antigen (Ag)-binding region. The present sequence represents an anti-cDc cynomolysus monkey Ig heavy chain variable region. An anti-CD4 antibody (Ab) comprising the light and heavy-chain variable regions encoded by DNA corresponding to the present sequence, and that of T91565, is also new. The Abs are useful for human therapy, especially of tumours. Old world monkeys are sufficiently different from humans to allow Abs to be raised in these monkeys, and are sufficiently similar to humans to be raised in these monkeys, and are sufficiently similar to humans to avoid host anti-Ab immune responses when the Abs are introduced into
                                                                               05-MAY-1998 (first entry)
Monkey anti-CD4 heavy chain variable region protein sequence.
Monkey anti-CD4 heavy chain variable region; monkey; baboon;
macaque; immunoglobulin; heavy chain variable region; chimpanzee; h
lymphoma; AIDS; autoimmune disease; inflammatory disease; transplan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric antibodies for he chimpanzee immunoglobulin antigen-binding region Example 3; Fig 13; 46pp; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-CD4 cynomolgus monkey immunoglobulin heavy chain variable region Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig; chimpanzee; chimeric antibody; human therapy; Old World monkey;
                                                tumour; antibody.
                                                                                                                                                                                                                                                                                                                                            W43430 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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25-JUL-1991; US-735064.
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25-JUL-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LKYLH-WLLYWGQGVLVTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AARPHRYEDYWGQGTLYTYSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGKGLEWIGEINHS-GSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGKGLEWIGYIYGSGGGTNYNPSLNNRVSISIDTSKNLFSLKLRSVTAADTAVYYCASNI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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77.3%;
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orld monkey
s an anti-CD4
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                                                                                                                            hybrid;
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cynomolgus

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PA (IDEC.) IDEC PHARM CORP.
PI Hanna N, Newman RA, Raab RW;
PI Hanna N, Newman RA, Raab RW;
PR Hanna N, Newman RA, Raab RW;
PR N-SDB; V05695.

PN Nucleic acid encoding hybrid antibody - comprising monkey
PT antigen-binding region and human or chimp constant region from an
CC anti-human CD4 immunoglobulin raised in cynomolgus monkeys. The coding
CC sequence was PCR amplified and used in the construction of a recombinant
CC anti-hody comprising: (1) an old World monkey Ig antigen-binding region;
CC and (ii) a human or chimpanzee Ig constant region. The hybrid antibodies
CC can be used as passive or active therapeutic agents against human
CC diseases, e.g. B-cell lymphoma, AIDS, autoimmune and inflammatory
CC diseases, transplant rejection or tumours, or for producing therapeutic
CC and diagnostic conjugates. Although evolutionary distant monkeys are
CC used to raise antibodies against human antigens, they are sufficiently
CC similar that they produce antibodies similar to human antibodies, such
CC anti-antibody response is stimulated.
SQ Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5693780-A.
02-DEC-1997.
07-JUN-1995;
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Peptide
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1992;
  61
                            60 PGKGLEWIGEINHS-GSTNYNPSLKSRYTISVDTSKNQFSLKLSSYTAADTAVYYCAREI 118
                                                                                                  PGKGLEWIGYIYGSGGGTNYNPSLNNRVSISIDTSKNLFSLKLRSVTAADTAVYYCASNI 120
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US-481869.
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20. .140
/note= "mature protein"
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1. .19
                                                                                                                                                                                                             71.7%; Score 536.5; DB 1; 77.3%; Pred. No. 5.7e-38; vative 7; Mismatches 22;
                                                                                                                                                                                                                                                                  Length 140;
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Best Local Similarity 77.3
Matches 109; Conservative
119 AARPHRYFDYWGQGTLVTVSS 139
| : ||||| |||||
121 LKYLH-WLLYWGQGVLVTVSS 140
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Search completed: July 26, 2000, 14:01:26 Job time: 2765 sec

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Result
No.
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              number of hits satisfying chosen parameters:
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1: pir1:*
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A;Molecule type: DNA
A;Residues: 1-140 <GRI>
A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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# ALIGNMENTS

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C;Access...
R;Harindranath, N.
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R;Reference to the EMBL Data Library, ...
A;Reference number: $78051
A;Reference number: $78052
A;Molecule type: mRNA
A;Residues: 1-140 <HAR>
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: $78052; $23717
                                                                                                                                                                                                                                                                                                 Ig_heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
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Best Local Similarity
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Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region
A;Reference number: A36876; MUID:94119917
A;Accession: I37782
                                           Ig heavy chain V region - hum C: Species: Homo sapiens (man)
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A;Residues: 15-111 <HAW>
A;Residues: 15-111 <HAW>
A;Residues: 15-111 <HAW>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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A; Title: Complete
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:ResIdues: 1-140 <RES>
:ResIdues: 1-140 <RES>
:Chas:references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
:Chas:references: EMBL:X67906; PID:gat.Y67906; PID:
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22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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                                                                            human (fragment)
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Pred. No. 2e-49;
6; Mismatches 12;
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Pred. No. 7.9e-51;
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operal, Reference number: S31585
A;Accession: S31676
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S31676
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R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate A;Reference number: S31585

A;Accession: S31586
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A; Residues: 1-137 <CUI>
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A; Residues: 1-139 <CUI>
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Best Local Similarity
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Best Local
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                                        121 RPHRY-FDYWGQGTLVTVSS 139
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                                                                                                          61 GKGLEWIGEINHSGSTNYNPSLKSRYTISVDTSKNQFSLKLSSYTAADTAVYYCAREIAA 120
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APLMYGMDVWGQGTTVTVSS 137
                                                                                 GKGLEWIGRIYTSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARD----
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                                                                                                                                                                     MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPA 60
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82.9%;
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Pred. No. 8.3e-46;
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Pred. No. 3.7e-46;
4; Mismatches 20;
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RESULT 6 \$13519 Ig heavy chain V region precursor -C:Species: Homo sapiens (man)

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A:Status: preliminary
A:Status: preliminary
A:MORECULE type: mRNA
A:MOLECULE: 1-147 - CMORE
A:Residues: 1-147 - CMORE
A:Cross references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
A:Cross references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Reywords: heterotetramer; immunoglobulin
F:41-125/Domain: immunoglobulin homology <IMM>
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A;Accession: S13519
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 18-115 <HAW>
A; Cross-references: EMBL: X54445
A; Cross-references: EMBL: X54445
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
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F;32-115/Domain: immunoglobulin homology <IMM>
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A; Reference number: S78051
A; Accession: S78055
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C;Accession: Sls
                                                                                                                                                              Query Match
Best Local S
Matches 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID:g37818: Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, Immunol. 3, 865-875, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reference number: S23716; MUID:92031262
Accession: S23720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA Residues: 1-145 <HAR>
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Best Local Similarity
Matches 116; Conser
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                                                                                                                                                                Local Sim
hes 116;
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  KGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREIAA- 120
                                                                                            HLMFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSF-SGYYWSWIRQPPG 61
                                                                      HLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPG
                                                                                                                                                                                   Similarity
                                                                                                                                                                Conservative
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                                                                                                                                                                                 77.0%;
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82.3%;
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, 1991
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Pred. No. 9.9e-46;
5; Mismatches 17;
                                                                                                                                                           Score 576; DB 2; Length 145; Pred. No. 5.7e-45; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                #status predicted <MAT>
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                                                                                                                                                              Indels * 10;
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A;Cross-references: EMBL:235492; NID:g517254; PIDN:CAA84625.1; PID:g517255 (;Superfamily: immunoglobulin v region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin C;Reywords: heterotetramer; immunoglobulin F;15-97/Domain: immunoglobulin homology <IMM>
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R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in A;Reference number: $47009
A;Accession: $47010
                                                                                                                                                                                                C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S47010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1-19/Domain: signal sequence #status predicted <SIG>F;20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <MAT>F;20-117/Region: V segment
F;35-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 3, 181-189, 1985
A;Title: A cloned human immunoglobulin heavy chain gene with
A;Reference number: A02101; MUID:85205332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain precursor V-II region (ARH-77) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
A; Molecule type: mRNA
A; Residues: 1-126 <MAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;42-115/Disulfide bonds: #status predicted
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A;Map position: 14q32.33-14q32.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-146 < KUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Kudo, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the sequence was determined from the differentiated A;Note: the authors translated the codon GGG for residue 17
                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                    Ig heavy chain V4.21-UniqueD-J5 region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:IGHV@
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKHLWFLLLWCQLPDVGVLSQVQLQQWGAGLVKPSETLSLTCAVFGGSFSGYYWSWIRQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREIA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPHRYFDYWGQGTLVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.4%;
78.1%;
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Pred. No. 1.5e-44;
5; Mismatches 20;
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                                                                                                                               human anti-DNA
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F;47-129/Domain: immunoglobulin homology <IMM>

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A;ACCESSAUM: FREIMINARY
A;Status: preliminary
A;MoLecule type: mRNA
A;Residues: 1-155 <CHA>
A;Residues: 1-155 <CHA>
A;CROSS-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library. December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of a A;Recession: S31509
A;Recession: S31511
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A:Residues: 1-139 <CUI>
A:Residues: 1-139 <CUI>
A:COOSS references: EMBL:Z14194; NID:g30975; PIDN:CAA78563.1; PID:g30976
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
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A;Description: Mechanisms that generate human immunoglobulin diversity operate from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: S31696
R; Cuisinier, A.M.; (
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A;Accession: S31696
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Best Local S
Matches 110
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Best Local Similarity
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A; Molecule type: mRNĀ
A; Residues: 1-146 <HUG>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                     R; Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J. Blochem. J. 268; 135-140, 1990
A; Title: Nucleotide sequences and three-dimensional modelling A; Reference number: S09710; MUID:90262535
A; Accession: S09711
                                                                                                                                                                              Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996 C;Accession: S09711
                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-155 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: Dominance of clonotypic patterns and variable gene usage of A;Reference number: S31509
A;Accession: S31512
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Best Local Similarity
Matches 112; Conserv
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112; Conservative
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MBL Data Library, December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.38;
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77.8%;
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Pred. No. 8.1e-44;
8; Mismatches 19
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Pred. No. 2.3e-44;
7; Mismatches 18
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F;34-118/Domain: immunoglobulin homology <IMM>

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Ig heavy chain V-IV region - human (fragment)
c;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuux
Eur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphol
A;Reference number: A49028; MUID:92008140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 1-231 <LEO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <IMM>
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                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-143 <TIM>
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F;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, Reference number: A23746; MUID:91131575
A;Accession: B23746
A;Status: preliminary
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                                                                                                                                                                      A; Accession: B49028
Cross references: GB:S64473; NID:9236906; PIDN:AAB20012.1; PID:9236907; PERPENDENTAL SOURCE: X-linked agammaglobulinemia patients, B lymphoblastoid; Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIP:64472); Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
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Pred. No. 1.4e-43;
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Pred. No. 3.9e-43;
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F;15-97/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 86.0%;
Matches 111; Conservative
 121
                            131
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                                                    PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGPIVVVPAAMRGRGWDYGMDVWG
QGTTVTVSS 129
                                                                  PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-----EIAARPHRYFDY----WG 130
                        QGTLVTVSS 139
                                                                                                                                                            Score 554.5; DB 2;
Pred. No. 4.8e-43;
1; Mismatches 8;
                                                                                                                                                              Indels
                                                                                                                                                                                       Length 143;
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Search completed: July 26, 2000, 14:21:22 Job time: 3442 sec

#### Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution. July 26, 2000, 14:03:14; Search time 12.18 Seconds (without alignments) 353.652 Million cell updates/sec 5 homo sapien 2 mus musculu 7 mus musculu 6 mus musculu 6 mus musculu mus musculu mus musculu mus musculu mus musculu rattus norv 7 mus musculu 3 mus musculu 8 mus musculu 0 mus musculu 0 mus musculu homo sapien homo sapien mus musculu mus musculu mus musculu homo sapien xenopus lae mus musculu xenopus lae mus musculu homo sapien homo sapien RESULT: 2 HY2E HUMAN ID HY2E HUMAN AC P01824; DT 21-JUL-1986 DT 21-JUL-1986 DT 15-JUL-1999 δÃ 밁 Š 밁 Q ESULT 1 HV2I\_HUMAN TO HV2I\_HUMAN D HV2I\_HUMAN D HV2I\_HUMAN TO 01-JAN-1988 (Rel. 06, Created) TO 1-JAN-1988 (Rel. 06, Last sequence update) TO 1-JAN-1988 (Rel. 38, Last annotation update) TO 1-JAN-1988 (Rel. 06, Created) TO 1-JAN-1988 (Rel. 06, Last annotation update) TO 1-JAN-198 (Rel. 18, Last annotation update) TO 1-JAN-199 (Rel. 18, Last annotation update) TO 1-JAN-199 (Rel. 18, Last annotatio Query Match Best Local Similarity Matches 114; Conserv DOMAIN DOMAIN DOMAIN DISULFID NON\_TER SEQUENCE SIGNAL 121 120 ARPHRYFDY-----WGQGTLVTVSS 139 61 60 <u>ب</u> $\vdash$ 0 000 0000 0 RGGWNDVDYYYGMDVWGQGTTVTVSS 146 PGRGLEWIGEINHSGSTNYKTSLKSRVTISLDTSKNLFSLKLSSVTAADTAVYYCARGLL 120 PGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREIA 119 76.4%; milarity 78.1%; Conservative 146 (Rel. (Rel. (Rel. 516644465567 **&** STANDARD 38, 146 117 127 146 146 16228 Created) Last sequence Last anno MW; sequence up annotation HYZB\_HUMAN HY51\_MOUSE HY03\_MOUSE HY18\_MOUSE HY19\_MOUSE HY21\_MOUSE HY21\_HUMAN HY2C\_HUMAN HY2C\_HUMAN HY2C\_HUMAN HY2C\_HUMAN HY04\_MOUSE HY11\_MOUSE HY11\_MOUSE ū IG HEAVY CHAIN V SEGMENT. D SEGMENT. J SEGMENT. BY SIMILARITY. Score 571.5; DB 1 Pred. No. 4.7e-48; 5; Mismatches 20 PRT; 8D7FD52BB218171F CRC64; ALIGNMENTS update) 129 A DB 1; V-II 20; REGION Length Indels Euteleostomi; Ø Homo. P01815 P06330 P01747 P01787 P01788 P01792 P01769 P01748 P01786 P01786 P01786 novel direct-146; 7; mus musculu mus musculu mus musculu mus musculu mus musculu mus homo sapien homo Gaps musculu musculu 60 59

Minimum Maximum

seq

length: 0 length: 1000000

Title: Perfect score:

US-09-203-768A-2 748 1 MKHLWFFLLLVAAPR

MKHLWFFLLLVAAPRWVLSQ.....ARPHRYFDYWGQGTLVTVSS

Scoring table:

BLOSUM62 Gapop 10.0 ,

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ched:

85661 segs,

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number DB DB

of.

hits satisfying chosen parameters:

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen

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Database

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Post-processing: Minimum Match Maximum Match Listing first

summaries

Result No.

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P06331 Description SUMMARIES

571.5 411.5 408 397.5

HV60\_MOUSE

HV02\_XENL

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1\_MOUSE

332 332 332 332 332 332

HV3D\_HUMAN
HV42\_MOUSE
HV13\_MOUSE
HV02\_MOUSE
HV12\_MOUSE

HV2H\_HUMAN

HV22\_MOUSE HV44\_MOUSE HV39\_MOUSE HV01\_RAT

HV45\_MOUSE

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PIR, A02099; D2HUWA.

HSSP; PO1825; 7FAB.

PFAM; PF00047; 19; 1.

Immunoglobulin V region.

Immunoglobulin 29

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P01822;

P01821-1986 (Rel. (
                                                                                                                                                                                             Jilka R.L., Pestka S.;
Jilka R.L., Pestka S.;
Jilka R.L., Pestka S.;
Jilka R.L., Pestka S.;
Jimnunoglobulin heavy chain.";
Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
                                                                                  SEQUENCE OF 1-21.

MEDLINE; 79148758.

Schechter I., Wolf O., Zemell R., Burstein "Structure and function of immunoglobulin g Fed. Proc. 38:1839-1845(1979).
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                        SEQUENCE OF 19-136. MEDLINE; 74170779.
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Rinfret A., Horne C.,
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11-JUL-1986 (Rel. 23, Last sequence update)
15-JUL-1992 (Rel. 23, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION MOPC 315 PRECURSOR.
1915 musculus (Mouse).
1847YOta; Metazoa; Chordata; Craniata; Verte;
1847YOta; Metazoa; Chordata; Sciurognathi; M
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c. Natl. Acad. S
MISCELLANEOUS:
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Pred. No. 8.4e-33;
4; Mismatches 21;
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WAS ISOLATED FROM
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a heavy
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                                                                                                         precursors.";
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Francis

S.H.,

Leslie

R.G.Q.,

Hood L.,

Eisen H.N.;

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RESULT 4
HY2G_HMAN
ID HY2G_H
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DT 21-7UL
DT 21-7UL
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DT 15-WEL
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Best Local S
Matches 85
                                       HV2G_HUMAN STANDARD; PI
PO1825;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seque
15-JUL-1999 (Rel. 38, Last annot
IG HEAVY CHAIN V-II REGION NEWM.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hood L., Margolles M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
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MEDLINE; 77244979
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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PFAM; PF00047; 1g;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Amino-acid sequence of the variable region of the heavy (alpha) chain of a mouse myeloma protein with anti-hapten activity."; proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
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                                                                                                                                                                                                                                                             MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSF-SGYYWSWIRQP
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V region;
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t annotation
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G -> GG (IN CAA30727).
G -> H (IN REF. 2).
GY -> YG (IN REF. 4).
N -> D (IN REF. 4).
MISSING (IN REF. 4).
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Pred. No. 1.9e-32;
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COMPLEMENTARITY-DETERMINING
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                                                    on update)
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Best Local Similarity
Thes 77; Conserv
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION M315 PRECURSOR.
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SEQUENCE.
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PIR; A02100; G1HUNM
PDB; 7FAB; 31-JAN-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 77242302.
Poljak R.J., Nakashima Y., Chen B.L.,
Poljak R.J., Nakashima Y., Chen B.L.,
"Amino acid sequence of the VH region
immunoglobulin (IgG New).";
Biochemistry 16:3412-3420(1977).
                                                                                                                                 MOUSE
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PFAM; PF00047; 1g; 1.
Immunoglobulin V region
         STRAIN-BALB/CJ;
MEDLINE; 89279149.
                            SEQUENCE FROM N.A.
                                                       Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                     HV60_MOUSE
                                                                                                                                                                                                                                                                                          SEQUENCE
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                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preliminary refinement
                                                                                                                                                                     61
                                                                                                                                                                                 80 PSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAREIAARPHRYFDYWGQGTLVTVSS 139
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                                                                                                                                                                     TPLRSRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARNLIA - - - GCIDVWGQGSLVTVSS
                                                                                                                                                                                                        QVQLEQSGPGLVRPSQTLSLTCTVSGSTFSNDYYTWVRQPPGRGLEWIGYVFYHGTSDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an immunoglobulin new at 2.0-A Chem. 253:585-597(1978).
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Malipiero U.V.,
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                                                                                                                       STANDARD;
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Rodentia;
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PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                             19;
Lebecque S.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structural
                                                                                                                                                                                                                                                      Score 397.5;
Pred. No. 1.
                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                       PRT;
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                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resolution.";
                                                                                                                                                                                                                                           5; DB 1;
1.6e-31;
nes 21;
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Gearhart P.J.;
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Best Local S
Matches 75
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PIR; JT0509; HVMS31.
PFAM; PF00047; ig; 1.
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SEQUENCE
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                                              PIR; A02094; G2MS14.
PFAM; PF00047; 1g; 1.
Immunoglobulin V region;
                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                  MOUSE STANDARD; PRT; 144 AA.
P01819; P15-1916 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION MOPC 141 PRECURSOR.
                                                                                                                                                                                                                                                                   Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa "Two types of somatic recombination are necessary for of complete immunoglobulin heavy-chain genes.";
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 81012133. Sakano H., Maki R.,
                                                                                                                                                                                                                        Nature 286:676-683(1980).
-!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa; (
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Pred. No. 6.9e
15; Mismatches
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COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
BY SIMILARITY.
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                        IG HEAVY CHAIN V REGION MOPC
8E47A7CB3706D30A
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5.9e-29;
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 CRC64
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Query Match Best Local Similarity

49.48;

Score 369.5; DB 1; Pred. No. 9.9e-29;

Length 144;

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RESULT 7
HV47_M
ACCOLORS
ID HV47_M
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ACCOLORS
IC 10123
IC 11-JUL
IC 15-JUL
IC 15-JUL
IC 16-JUL
IC 16-JUL
IC MARMAL
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                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUI-1999 (Rel. 38, Last annotation update)
15-JUI-1999 (Rel. 38, Last annotation update)
16 HEAVY CHAIN V REGION XIG14 PRECURSOR (FRAGMENT).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                    HV02_XENLA
P20957;
                                                                                                                                                                                                                                                                                                                                                              XENLA
                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A02098; G2MS60.

PEAM; PE00047; 19; 1.

Immunoglobulin V region; Antiarsonate antibody.

NON_TER 113 113

SEQUENCE 113 AA; 12734 MW; 38DC0E0E3F5075B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 84024551.
"Juszczak E.C., Margolies M.N.;
"Amino acid sequence of the heavy chain variable region from 1
mouse anti-arsonate monoclonal antibody 36-60 bearing a minor
                                                                        Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 22:4291-4296(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-A/J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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21-JUL-1986 (Rel. 01,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Sin
hes 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -JUL-1986 (Rel. 01, Last sequence update)
-JUL-1999 (Rel. 38, Last annotation update)
-HEAVY CHAIN V REGION 36-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANT:
MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRI
IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREIAARPHRYFDYWGQGTLYTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQLQESGPSLVKPSQTLSLTCSVTGDSITSDYWNWIRKFPGNKLEHMGYISYSGSTYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
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                                                                     Xenopus
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                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 359.5; DB 1;
Pred. No. 6.8e-28;
9; Mismatches 23;
                                                                                                                                                                                                                                                                                                                         PRT;
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I REPRESENTS A SE
SONATE RESPONSE (
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Query Match
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                                                                                                                                                                                                                                                                                                                                                           MOUSE STANDARD; PRT; 116 AA. P18532; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 1G HEAVY CHAIN V REGION 1B43 PRECURSOR.
                                                                                                                                                               Levy N.S., Malipiero U.V., Lebecque "Early onset of somatic mutation in the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
III MISCELLANEOUS: THIS SEQUENCE BEI
                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                  PIR; JT0508; HVMS1B.
PFAM; PF00047; 1g; 1
                                                                                                                                                                                                                                                   STRAIN-BALB/COMEDLINE; 89279
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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NON_TER
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PIR; B31
                                                                                                                 .mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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PFAM; PF00047; 1g; 1.

Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schwager J., Mikoryak C.A., Steiner L.A.;
Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
From cDNA sequence: implications for evolution of immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDYWGQGTMVTVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIGVIATGGSTAIADSLKNRVTITKDNGKKQVYLQMNGMEVKDTAMYYCAREYASGYN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIGEINHSGSTNYNPSLKSRYTISVDTSKNQFSLKLSSYTAADTAVYYCAREIAARPHRY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFIFMFFSPSCILSQT-LQESGPGTVKPSESLRLTCTVSGFELSSYHMHWIRQPPGKGLE
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                                                                                                                                                                                                                                                   89279149
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   Conservative
                                                                                                                   19;
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                                                                                                             Signal.
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FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
                                            FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 359.5;
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION XIG14
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                                                                               HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                               BELONGS TO
                                                                                                                                                                                                            S.G., Gearhart
immunoglobulin
                                                                               CHAIN V REGION
                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .3e-28;
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                                                                                                                                                               THE
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                                                                                                                                                              VH3660 SUBFAMILY.
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VH ge
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Best Local
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21-JUL-1986 (Rel. 01, 0
21-JUL-1986 (Rel. 01, 1
15-JUL-1999 (Rel. 38, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
NON_TER
SEQUENCE
                                                                                 DOMAIN
DISULFID
                                                                                                                                                                                                  EMBL; J00529; AAA38170.1; -. PIR; A02034; MHMS18. PFAM; PF00047; ig; 1. Immunoglobulin V region; Sig
                                                            SEQUENCE
                                                                                                                                                       DOMAIN
                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                               use by non-profit institutions a modified and this statement is not
                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                      antibodies: somatic mutation evident in a gamma Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 81234548.
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                            CHAIN
                                                                                                                                DOMAIN
                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                    pntities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                         MAIN
                                                                                                                                                                                                                                                                                                                                                                                                            Heavy chain variable region contribution to the NPb family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VO7
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                                                                                                                                                                                                                                                        send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                               MAKING ANTIBODIES TO THE
                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMOUSE
                                                                                                                                                                                                                                                                                                                                                     (NPB ANTIBODIES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRVLILLCLFTAFP-GILSDVQLQESGPDLVKPSQSLSLTCTVTGYSITSGYSWHWIRQF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSF-SGYYWSWIRQP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGNKLEWMGYIHYSGNTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 60.7
71; Conservative
   l Similarity
67; Conser
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116
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41
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el. 38, Last annotation update)
V REGION B1-8/186-2 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Α.,
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116
13158 MW;
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                                                                                                                                                                            139
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9 4 8 5
                                                         15419 MW;
                                                                                                                                                                                                                                                                                           institutions as long
             50.48;
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                                                                                                                                                                                                  Signal.
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Score 330; DB 1;
Pred. No. 5.7e-25;
2; Mismatches 42
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6; Mismatches
                                                                               JH2 SEGMENT.
BY SIMILARITY.
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Pred. No. 2
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                                                                                                         D SEGMENT.
                                                                                                                  COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3.
                                                                                                                                        COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
                                                                                                                                                                FRAMEWORK
                                                                                                                                                                           IG HEAVY CHAIN V REGION B1-8/186-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                         1B57DD4FD0C9F465 CRC64;
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.7e-26;
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                        Length ·139;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HV11_MO
P01755;
                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                     PFAM; PF00047; ig; Immunoglobulin V re
                                                                                                                                                                                                                                                                                                                                                                EMBL; J00539; AAA38172.1; PIR; A02038; G2MS43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bothwell A.L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 81234548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V REGION S43 PRECURSOR.
                                                                                                                                                                                                                 DOMAIN
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                                                               LLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWI
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GRIDPNSGGTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCAR---YRLGRYF
                        GEIN-HSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREIAARPHRYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEIN-HSGSTNYNPSLKSRVTISVDTSKNOFSLKLSSVTAADTAVYYCAREIAARPHRYF
                                                LFLAATATGVHSQVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       odies: somatic m
24:625-637(1981)
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                                                                                                         66;
                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long as its content and this statement is not removed. Usage by a
                                                                                                         Conservative
                                                                                                                                                                         A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
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                                                                                                                                                                                                                                                                                                                                     Signal.
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                                                                                                                                                                         Œ;
                                                                                                        22;
                                                                                                                 Score 329; DB 1
Pred. No. 7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contribution evident in a
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                                                                                                                                                                                                                           FRAMEWORK 3.
D SEGMENT.
                                                                                                                                                                                                   JH2 SEGMENT.
BY SIMILARIT
                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                      FRAMEWORK 2
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                                                                                                         Mismatches
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                                                                                                                               DB 1;
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                                                                                                                               Length 137;
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124
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DYWGQGTLVTVSS

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125 DYWGQGTTLTVSS

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Best Local Similarity
Matches 66; Conserv
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/_MOUSE
HV37_MOUSE
P01807;
                                                                                                                                                                                                                                                                                                                                                                         HV62_MOUSE
P18533;
01-NOV-1990
                       the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
PIR; JT0510; HVMS73.
                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V REGION 733 PRECURSOR.
                                                                                          MEDLINE: 89279149.
Levy N.S., Malipiero U.V., Lebeco "Early onset of somatic mutation"
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
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21-JUL-1986 (Rel. 01, Last sequence up. 15-JUL-1999 (Rel. 38, Last annotation IG HEAVY CHAIN V REGION X44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mao D.N., Ruddkoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in
immunoglobulin heavy chains from anti-galactan myeloma proteins
its potential role in generating diversity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ao D.N., Rudikoff S., Krutzsch H., 1
Structural evidence for independent
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EDLINE; 79223895
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mmunoglobulin V region.
119 119
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       PF00047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13246 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.98;
                                                                                            Lebecque
tation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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Pred. No. 7.5e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC34FC8F31CD41B3 CRC64;
                                                                                          S.G., Gearhart
immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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.5e-25;
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                                                                                          P.J.;
VH ge
                                                                                          genes during
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RESULT 15
HV40\_MOUSE
ID HV40\_MOUSE
AC P01810;
DT 21-JUL-1986

STANDARD;

PRT;

119

(Rel.

01, Created)

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118 S 118

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61 TPSLK 139 S 139 Š

79 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREIAARPHRYFDYWGQGTLVTVS 138

TPSLKDKFIISRDNAKNTLYLOMSKVRSEDTALYYCAR---LGYYGYFDVWGAGTTVTVS

117

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HV38_M
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Best Local S
Matches 68
                                                                                                  Matches
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Best Local Similarity
                                                                                                                                                                                                                 HSSP; PO1810; 2FBJ.
PFAM; PF00047; 1g; 1.
Immunoglobulin V region.
NON_TER 119 119
SEQUENCE 119 AA; 13169 M
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DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAO D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin
SIGNAL
                                                                                                                                                                                                                                                                                                                                        PIR; A02078; AVMST6.
                                                                                                                                                                                                                                                                                                                                                                                   complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 03, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG HEAVY CHAIN V REGION T601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HV38_MOUSE
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EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;83
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117
                                                                                               Conservative
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115 B
117
13223 MW;
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Rodentia;
                                                                                                                      43.6%;
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                                                                                                                                                                                                                      WW;
                                                                                                  16;
                                                                                          Score 326; DB 1;
Pred. No. 1.2e-24;
6; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 326.5;
Pred. No. 1e
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PIG
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                                                                                                                                                                                                                      BC38CC84E6EA00E8 CRC64;
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                                                                                                                                        Length 119;
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                                                                                               Indels
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Best Local Similarity
Matches 65; Conserv
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STRAND
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PDB; 2FBU; 15-OCT-90
PFAM; PF00047; 19; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE: 88217852.
Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in
immunoglobulin heavy chains from anti-galactan myeloma proteins and
its potential role in generating diversity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION J539.
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118 A 118
                                       139 S 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tudy at 2.6-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ivies D.R.;
The galacta
                                                                                 61
                                                                                                                  79
                                                                                                                                                                              20 QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEIN-HSGSTNY 78 :|:|: | ||:|| ||:|| ||:||: ||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDS GALACTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                                        TPSLKDKFIISRDNAKNSLYLOMSKVRSEDTALYYCAR---LHYYGYNAYWGQGTLVTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      galactan-binding immunoglobulin Fab J539: an X-ray diffraction
                                                                                                                NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREIAARPHRYFDYWGQGTLVTVS 138
                                                                                                                                                          EVKLLESGGGLVQPGGSLKLSCAASGFDFSKYWMSWVRQAPGKGLEWIGEIHPDSGTINY 60
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region;
                                                                                                                                                                                                                                                                                                                            116
13240 MW; 577B4F1DB675C1F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  542
542
544
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103
                                                                                                                                                                                                                                     43.4%; Score 325; DB 1; 53.7%; Pred. No. 1.4e-24; ative 19; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-structure
                                                                                                                                                                                                                                     33; Indels
                                                                                                                                                                                                                                                                            Length 119;
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Search completed: July 26, 2000, 14:25:25 Job time: 1331 sec

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Result
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  328.5
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## ALIGNMENTS

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Qy 118 IAARPHRYEDYWGQGTLVTVSS 139 :	Qy 59 PPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR-E 117 	QY 1 MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQ 58	Query Match 73.8%; Score 552; DB 4; Length 150; Best Local Similarity 76.8%; Pred. No. 4.2e-49; Matches 109; Conservative 11; Mismatches 14; Indels 8; Gaps 3;	SEQUENCE 150 AA;	FT CHAIN 20 >150 VH4 HEAVY CHAIN VARIABLE REGION. FT NON_TER 150 150	SIGNAL 1 19	HSSP; P01825; 7FAB.	RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.  DR EMBL; AF103795; AAC79084.1;	Behcet's patient with arthritis.";	"Clonal proliferation of IgM secreting		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	Homo sapiens (Human).	IGM	VH4 HEAVY CHAIN VARIABLE	01-NOV-1999 (Trembire).	DT 01-MAY-1999 (TrEMBLrel 10, Created)	095973;	ID 095973 PRELIMINARY; PRT; 150 AA.	O95973 •

PRELIMINARY;

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Best Local Similarity
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Best Local Similarity
Matches 61; Conserv
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075739;
01-NOV-1998
01-NOV-1998
1-NOV-1998
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075725;
01-NOV-1998
01-NOV-1998
01-NOV-1999
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human IgA and IgM secreting intestinal plasma cells carry mutated VH region genes.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ009538; CAA08743.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Human IgA and IgM secreting intestinal plasma cells carry heavily utated VH region genes.";
"Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ009522; CAA08729.1; -.
HSSP; P01825; 7FAB.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FISCHER M., KUEPPERS R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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-NOV-1998 (TIEMBLIEL 08, Last sequence update)
-NOV-1998 (TIEMBLIEL 08, Last annotation update)
HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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TAVYYCAREI-AARPHRYFDYW
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                                                                                                                                                                                                                                                                                                                                                     78 AA;
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(Tremblrel. 08, Last sequence update)
(Tremblrel. 12, Last annotation update)
ain variable region (fragment).
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9031 MW;
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Pred. No. 1.3e-26;
7; Mismatches 13;
                                                                                                                                                  Score 312; DB 4;
Pred. No. 5.8e-25;
B; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                 05D273B9 CRC32;
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Best Local S
Matches 63
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075743;
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TREMBLREL. 0
1G HEAVY CHAIN VARIABLE R
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LICHTENSTEIN A.K., BERENSON J.R.;
"A CD10-positive subset of malignant cells is identified in
myeloma using PCR with patient-specific immunoglobulin gene
Leukemia 9:1948-1953(1995).
EMBL; S80860; AAD14339.1; -.
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Q9Y509;
01-NOV-1999
01-NOV-1999
                                                                         FISCHER M., KUEPPERS R.;
"Human IgA and IgM secreting intestinal plasma cells carry mutated VH region genes.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ009543; CAA08747.1; -.
                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
   SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                    PISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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9 (Tremblrel.
9 (Tremblrel.
N (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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   8667
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REGION (FRAGMENT).
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Pred. No. 8.1e-24;
8D5C330F CRC32;
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primers.";
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Best Local S
Matches 56
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Best Local
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01-MAY-1999 (TIEMBLIEL. 10, Last sequence update)
01-MAY-1999 (TIEMBLIEL. 10, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGME
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Furtheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUELLER J.P., GIANNONI M.A., HARTMAN S.L., ELLIOTT E.A., SQUINTO S.P. MATIS L.M., EVANS M.J., "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases EMBL; U78801; AAD00293.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endothelial cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                     118 S 118
                             ISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                 139 S 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 YYCAREIAARPHRYFDYW 129
ISCHER M., KUEPPERS R.;
Human IgA and IgM secreting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                           61 TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRIVG---GYFDYWGQGTTLTVS
                                                                                                                                                                                                                                                                                                                                                    79 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREIAARPHRYFDYWGQGTLVTVS 138
                                                                                                                                                                                                                                                                                                                                                                                                            20 QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI-NHSGSTNY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 YWSWIROPPGKGLEWIGEINHSGSTNYNPSLKSRYTISVDTSKNOFSLKLSSYTAADTAV 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 287; DB 11;
Pred. No. 3.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 296.5; DB 4;
Pred. No. 2.1e-23;
6; Mismatches 13;
  intestinal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monoclonal antibodies with chimeric uman leukocyte binding to porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
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Best Local S
Matches 55
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Best Local Similarity
Matches 53; Conserv
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Submitted (JUL-1998) to the EN
EMBL; AJ009535; CAA08741.1; -.
HSSP; P01825; 7FAB.
NON_TER 1 1
NON_TER 88 88
SEQUENCE 88 AA; 10088 MW;
                       Q9Y298;
Q9Y298;
Q9Y298;
01-NOV-1999
01-NOV-1999
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NON_TER
SEQUENCE
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09Z1C6;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TREMBLrel. 10, Last annotation update)
01-MAY-1999 (TREMBLRel. 10, Last annotation update)
ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUELLER J.P., GIANNONI M.A., HARTMAN S.L., ELLIOTT E.A., SQUINTO S.P., MATIS L.M., EVANS M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IgG2/G4 constant regions
endothelial cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Humanized porcine VCAM-specific monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                116 SA 117
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                                                                                                                                                                                                                                                                                                                                                                                      NPSLKSRVIISVDISKNQFSLKLSSVTAADTAVYYCAR-EIAARPHRYFDYWGQGTLVTV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGS-TNY 78
                                                                                                                                                                                                                                                                                                                                                  NQRLKDKAILTVDKSSNTAYMQFSGPTSEDSAVYYCTRGEVS-----WFAYWGQGTLVTV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYCARGGGYHCIGGRCYRYYYNGVDVW 88
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55; Conserv
                                                                                                                                                                                                                                                                                                 139
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) (TrEMBLrel. 12, 0
) (TrEMBLrel. 12, 1
) (TrEMBLrel. 12, 1
TrEMBLrel. 12, 1
                                                                                                                         PRELIMINARY;
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                                                                     Created)
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Pred.
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Pred. No. 2e-20;
3; Mismatches
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No. 1.7
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.7e-21;
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PROTEIN

12, Last sequence update)
12, Last annotation updat (FRAGMENT).

update)

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                                                                                                                                                                                                                             FFT REFERENCE OF THE PROPERTY 
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095978
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   095978;
01-MAY-1999
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                      JOX A. ZANDER T., KUEEPERS R., IRSCH J., KANZLER H., KORNACKER BOHLEN H., DIEHL V., WOLF J.;
"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated w somatic mutations within the untranslated regions of rearranged class switch recombinated Ig genes.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                       Submitted (APR-1998) to the EMBL; AJ005570; CAA06599.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata;
utheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blood 92:496-506(1998)
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"Mechanism and kinetics of factor VIII inactivation:
"GG4 monocional antibody derived from a hemophilia A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
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MDWTWRVFCLLAVAP-GVHSQVQLVQSGAEIKRPGASVKVHCKTSGYVFTSYYIHWVRQP
                                             MKHLW-FFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDPDA-FDIWGQGTMVTVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARPHRYFDYWGQGTLVTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCA---V 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKGLEWIGEIN-HSGSTNYNPSLKSRYTISVDTSKNQFSLKLSSVTAADTAVYYCAREIA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP
                                                                                                l Similarity 43.3
61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 43.0
61; Conservative
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157
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 10, Last annotation update)
(PRECURSOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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157
17304 MW;
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16031 MW;
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                                                                                                                       34.3%;
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                                                                                              Score 256.5; DB 4;
Pred. No. 6.1e-19;
9; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 264.5; DB 4;
Pred. No. 8.9e-20;
1; Mismatches 53;
                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                           88468024 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B18EC39A CRC32;
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Best Local
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O43234; O1-010-1998 (TIEMBLIEL. 06, Created)
O1-JUN-1998 (TIEMBLIEL. 06, Last sequen
O1-MAY-1999 (TIEMBLIEL. 10, Last annota
RHEUMATOID FACTOR RF-ET13 (FRAGMENT).
Homo saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                          075741;
075741;
01-NOV-1998
01-NOV-1999
01-NOV-1999
IG HEAVY CHA
                                                                      mutated VH region genes.";
Submitted (JUL-1998) to the
EMBL; AJ009540; CAA08745.1;
HSSP; P01772; ZIG2.
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mol. Immunow. 0:0-0(1997).
EMBL; AF035802; AAB88534.1; -.
PFAM; PF00047; 1g; 1.
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                                                                                                                                                                          Human IgA and IgM secreting
                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                       ISCHER M., KUEPPERS R.;
                                                                                                                                                                                                                            ISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 LQQWGAGLLKPSETLSLTCAVYGGSFSGYYW--SWIRQPPGKGLEWIGEINHSGSTNYNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLKSRLTISKDTSKSQVVLTMTNMDPMDTATYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKESGPALVKPTETLTLTCTVSGFSLSNRRMGVSWIRQPPGKAVEWLAHIFANDEKSYST
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1999 (TrEMBLrel. )
Y CHAIN VARIABLE (
77 AA;
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llarity 52.1%;
Conservative 1
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  8734 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 08, Created)
08, Last sequence update)
12, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                          REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139
                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 245; DB 4; pred. No. 5.1e-18; was matches 28;
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  1F7F9E8E CRC32;
                                                                                                                                                                          intestinal plasma
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                                                                                                                                                                          cells carry heavily
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                                                                                                                                                                                                                                                                                                                                   Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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1;

Query Match
Best Local Similarity
Matches 48; Conserv

Conservative

6

Score 224.5; DB 4 Pred. No. 4.8e-16; 5; Mismatches 16

16;

11;

Gaps

DB 4;

Length Indels

30.0%;

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RESULT 14
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Matches 40; Conserv
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01-NOV-1998 (TIEMBLIEL 01
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01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                      "Human IgA and IgM secreting intestinal plasma cells camutated VH region genes.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AJ009524; CAA08731.1;
HSSP; P01772; 2IG2.
                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human IgA and IgM secreting intestinal plasma cells can mutated VH region genes.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases EMBL; AJ009527; CAA08734.1; -.
HSSP; P01772; 2IG2.
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Eukaryota: Drimates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-INTESTINE;
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FISCHER M., KUEPPERS R.;
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llarity 49.4%;
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Pred. No. 3.2e-15;
6; Mismatches 20;
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63DE158A CRC32;
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Search completed: July 26, 2000, 14:25:01 Job time: 1412 sec

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Matches 42; Conserv
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O75729;
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1999 (TrEMBLrel. 1
IG HEAVY CHAIN VARIABLE R
VH.
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SEQUENCE
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ009526; CAA08733.1; -.
HSSP; P01772; 2IG2.
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Eukaryota; Metazoa; (
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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              AVYYCARE--IAARPHRYFDYW 129
                                             YYWSWIROPPGKGLEWIGEINHSG-STNYNPSLKSRYTISVDTSKNQFSLKLSSVTAADT 109
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AVYYCVKDGVSANSVWDYFDYW
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9396 MW;
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REGION (FRAGMENT).
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82
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Pred. No. 7.2e-14;
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Pred. No. 2.4e-14;
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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 26, 2000, 14:01:26 ; Search time 33.21 Seconds (without alignments) 83.447 Million cell updates/sec

Title: Perfect score: US-09-203-768A-4 615

Sequence: 1 LWLPDTTGEIVMTQSPATLS.....QYNNWPPYTFGQGTKLEIKR 117

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

188963 segs, 23686106 residues

number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					SUMMARIES	
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No.	Score	Match:	Length	몂	Ħ	
<u>.</u>	538.5		234	<u>, ,                                  </u>	R52951	뚜 ;
2	52	85.0	129	<b>J1</b>	R38672	-Jk2. DŇA
ω	$\vdash$	•	117	H	W47582	n monoclonal
4	13.	•	349	μ	R12128	IgG aberrant
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σ	13.	•	414	Ь	R13111	IgG aberrant
7	09.	•	214	ட	Y06842	ID N
8	04.	•	134	Н	W11155	-lung tumour
9	499	•	129	$\vdash$	R41286	5 rearranged v
10	9	80.8	129	_	R38673	Vk-F105Jk. DN
11	ø	•	150	$\vdash$	W40069	
12	493.5	•	401	ب	R12129	ORF 1 of IgG light
13	90.	•	127	Н	W08946	Kappa light chain
14	489	•	115	_	R38648	V-kappa fra
15	œ	•	115		R62928	7,6
16	489	79.5	115	<b>,</b>	W41144	Human vkappa65.3 f
17	ထ	•	115	Н	W62182	Human DNA vkappa65
18	48	•	124	ч	W24539	Immunoglobulin r10
19	76.	•	120	<b>_</b>	W03946	DNA fragment vk65.
20	5	•	127	1	R50192	Light chain variab
21	74.	•	109	ب	W84096	V kappa
22	47	٠	110	_	W27545	G,
23	469.5	•	127	<u>.</u>	R50187	Light chain variab
24	٩	٠	128	μ.	P91001	P. aerugin
25	.5	٠	127	μ.	R50191	င္
26	465		115	ш	R38649	
27	· cn	•	115	_	R62929	Da vk6
28	ന	•	115	ட	W03947	vk65
29	m	•	115	ш	W41145	
30	46	75.6	115	_	W62183	Human DNA vkappa65
31	53	•	116	_	R38650	Human V-kappa frag
32	Ψ	75.4	116	ш	R62930	Human V-kappa vk65
33	63.	75.4	116	ب	W03948	DNA fragment vk65.

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Query Match 87.6 Best Local Similarity 87.9 Matches 102; Conservative

87.6%; Score 538.5; DB 1; Length 234; 87.9%; Pred. No. 2.5e-33; tive 9; Mismatches 4; Indels 1

Gaps

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Ü	4	ω	ເວ	F	5			37			
449	452	452	453.5	453.5	453.5	453.5	457.5	458	458	463.5	463.5
73.0	73.5	73.5	73.7	73.7	73.7	73.7	74.4	74.5	74.5	75.4	75.4
108	304	287	238	109	107	107	105	107	107	116	116
سو	<u>,,,</u>	H	Ь	<u>.</u>	Н	_	۳	μ,	<b>ب</b>	_	<b>—</b>
R54316	W40070	W40071	W83034	R50218	W58493	R38593	W31725	W01266	R54308	W62184	W41146
Anti-HIV gp120 imm		Human Hll-scFv con	Anti-Fas humanised	HSV glycoprotein F	Human kappa light	lambda	Alpha light chain	VL region of HIV n	Anti-HIV gp120 imm	Human DNA vkappa65	Human vkappa65.8 f

# ALIGNMENTS

밁 Ş 밁 

SKKKEDAR R38672 standard; Protein; 129 AA. R38672;

01-NOV-1993 (first entry) vk325-Jk2.

Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS; CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light; chain; epitope; immune deficiency.

Homo sapiens.

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RESULT
W47582
ID W4
AC W4
DT 2:
DE H1
KW AI
KW AI
KW AI
KW AI
OS H6
FH K6
FT R6
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The nucleotide sequence of F105 Vk (Q42707 - sequence differs other F105 Vk sequences given elsewhere in the specification) compared with germiline gene Humyk325 (Q42706), showing 97.7% similarity. By nucleotide sequence analysis, F105 appears to be derived from a member of the Vk III subgroup gene family. Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                  24-UN-1993.

10-DEC-1992: U10928.

10-DEC-1991: US-804652.

(DAND ) DANA FARBER CANCER INST INC.

(DAND ) NEW ENGLAND DEACONNESS HOSPITAL CORP.

(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                      W47582;
W47582;
22-JUN-1998 (first entry)
22-JUN-1998 (first entry)
22-JUN-1998 (first entry)
23-Monoclonal antibody; hybridoma
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peptide
                                                                                   W47582 standard;
                           Homo sapiens
                                                                                                                                                                                                                                                                                                                 and neutralises HIV, for monitoring HIV infection Disclosure; Page 74-75; 1
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N-PSDB; Q42706.
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                                                                                                                                 SSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS-SPYTFGQGTKLEIKR 129
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06-NOV-1990; U06426.
07-NOV-1989; US-432700.
(BRIM ) BRISTOL-MYERS SQUIB.
Shuford WW, Harris LJ, Raff H
WPI; 91-163947/22.
N-PSDB; Q11878.
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05-JUL-1996; JP-194095.
05-JUL-1996; JP-194095.
(MATS/) MATSUDA M.
(MOMI) MOXINAGA & CO L
WPI; 98-138233/13.
N-PSDB; V18674
Example 5; Fig 16; 104pp; English.

This sequence is deduced from the cDNA clone 489-Vk15 and inclu
the amino acid sequence beyond the first stop codon. The clone
incomplete, starting from the G of the ATG initiator codon, but
initial Met is given. Antibody molecules of the invention can
include one or two aberrant light chains containing a duplicate
                                                                                        Oligomeric immunoglobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of
                                                                                                                                                                                                                                                                          region
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1B1 IgG aberrant light chain with duplicated variable region immunoglobulin G; light chain; variable region; duplication;
                                                                                  class *
                                                                                                                                                                                                            WO9106305-A.
                                                                                                                                                                                                                                                                                                                region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a human monoclonal antibody (light chain variable region. The cDNA encoding the hMAb can be for commercial production of the hMAb. The cDNA was isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cDNA enceding human monoclonal antibody - us of antibody by hybridoma techniques commercially Claim 4; Fig 2; 8pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                               passive
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99; Conser
                                                                                                                                                                                                                                                                                                                                                                             immunity; group B streptococci.
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/label=
89. .98
/label=
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/note- "L'V 2"
244. 345
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131, .243
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Pred. No. 4.3e-32;
6; Mismatches 4
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be used
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Query Match 83. Best Local Similarity 85. Matches 100; Conservative
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                                                                                                                                                                                                                                                                                               the amino acid sequence beyond the first stop codon ("x" in the sequence represents a nonsense codon). The clone is incomplete, starting from the G of the ATG initiator codon, but the initial Met is given. Antibody molecules of the invention can include one or two aberrant light chains containing a duplicated variable region, to produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies watch just a single copy of the L'V region. The antibodies can be used to treat disease, e.g. the colorer avidity than antibodies watch just a single copy of the complete the copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than antibodies watch just a single copy of the colorer avidity than a copy of the colorer avidity than a colorer avidity than a copy of the colorer avidity than a copy of the colorer avidity t
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06-NOV-1990; U06426.

07-NOV-1989; US-432700.

(BRIM ) BRISTOL-MYERS SQUIB.

Shuford WW, Harris LJ, Raff
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R13018;
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N-PSDB; Q11878.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligomeric immunoglobulin(s) with high avidity for antigen(s) - formed by duplicating esp. variable region of light chain of IgG
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                                                                                                                                                                                                                               the placenta.
See also Q11879 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Fig 16; 104pp; English.
This sequence is deduced from the cDNA clone 4B9-Vk15 and includes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHRDNWPPGATFGGGTKVEIK 129
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Score 513.5; DB pred. No. 3e-31; 6; Mismatches 1
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Pred.
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No. 2.6
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RESULT Y06842 ID Y

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Y06842 standard;

Protein;

214 AA

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Local Similarity 85.

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Mismatches

Indels

Gaps

414; μ;

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TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPP-YTFGQGTKLEIK 116

NRATGIPARESGSGSGTDETLTISSLEPEDEAVYYCQHRDNWPPGATEGGGTKVEIK

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Query Match
Best Local s
Matches 100
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05-NOV-1999, U06426.
07-NOV-1989, US-432700.
(BRIM ) BRISTOL-MYERS SQUIB.
Shuford WW, Harris LJ, Raff HV;
WPI: 91-163947/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R13111;
10-MAR-1993 (revised)
01-AUG-1991 (first entry)
181 IgG aberrant light chain with duplicated variable region.
181 IgG aberrant light chain; variable region; duplication;
1mmunoglobulin G; light chain; variable region; duplication;
                                                                                                                 the amino acid sequence beyond the first stop codon ("x" in the sequence represents a nonsense codon). The clone is incomplete, starting from the G of the ATG initiator codon, but the initial Met is given. Antibody molecules of the invention can include one or two aberrant light chains containing a duplicated variable region, to produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies with just a single copy of the L'V region. The antibodies can be used to treat disease, e.g. infection by Streptococcus agalactiae. They are able to pass across
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R13111 standard; Protein; R13111;
                                                                        the placenta.
See also Q11879 and Q11880.
Sequence 414 AA;
                                                                                                                                                                                                                                                                                                 Oligomeric immunoglobulin(s) with high avidity for antigen(s) - formed by duplicating esp. variable region of light chain of IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
                                                                                                                                                                                                                                                    Example 5; Fig 16; 104pp; English.
This sequence is deduced from the cDNA clone 489-Vk15 and includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region
                                                                                                                                                                                                                                                                                    class
                                                                                                                                                                                                                                                                                                                               N-PSDB; Q11878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPP-YTEGQGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHRDNWPPGATFGGGTKVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LWLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVGSYLAWYQQKPGQAPRPLIYDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= variable region
/note= "L'V 2"
244. 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131. .243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- variable region /note- "L'V 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abel=
               83.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 AA.
               Score 513.5;
Pred. No. 3e
                           Length
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Y06842; 25-JUN-1999

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Best Local
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                                                                                                                                    Claim 12; Page 25; 46pp; English.

The present sequence is the light chain from the monoclonal antibody (MAb) TB2A36C3, which has high specificity against lung tumour antigens and is produced by an Epstein-Barr virus (EBV) transformed TB945 human B cell line. The MAb can be used to screen serum or tissue samples for a carcinoma associated antigen, lyse tumours in anti-tumour therapy (optionally with other agents) and activate immune competent CD4 or CD8 cells in a patient's blood
                                                        system.
Tumour draining lymph nodes obtained from a non-SCLC (small cell
                                                                                                                                                                                                                                                                                                                                                                                             Anti-lung tumour antigen monoclonal antibody TB2A36C3 - produc Epstein-Barr virus transformation of human lung cancer patient B-cells, useful in conjunction with other agents for lysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an antiHBs monoclonal antibody having t following properties: (A) CDR-3 of H chain variable region; (B) contains no Epstein Barr virus (EBV); (C) it binds at least one among human HBs antigens. The antiHBs monoclonal antibody is hig antibody titer and has low risk of EBV contamination. It can be prevent hepatitis C. sequence 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-lung tumour antigen monoclonal antibody light chain.
Light chain monoclonal; antibody; TB2A36C3; lung; tumour; EB
Epstein-Barr virus; TB945; human; B cell; screen; antigen;
Carcinoma; lysis; anti-tumour therapy; activation; CD4; CD8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T33664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mukerjee S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-SEP-1996.
18-MAR-1996; U03661.
16-MAR-1995; US-405034.
(MEDE/) MEDENICA R D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nomo sapiens.
W09628473-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W11155 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barr virus contamination
Disclosure; Page 9-10; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-HBs monoclonal antibody · produced without the risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 99-281053/24.
N-PSDB; X32826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-1997; 255705.
19-SEP-1997; JP-255705.
(NISN) NISSHINBO IND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J11089576-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AntiHBs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                 cancer) patient were cut into fine pieces and mashed. Post, isolated using CD19 coated immunomagentic beads, were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQXPGQAPRLLIYGASTRATGIPA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96-433764/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIVMTQSPATLSVSPGERATLSCRASQSVRSNLAWYQQKPGQAPRLLIYAASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102;
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)2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.88;
93.68;
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Pred. No. 3.2e-
1; Mismatches
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C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour; EBV;
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can be us
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                                                                       Query Match
Best Local :
                                                          Matches
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Best Local
                                                                                                                                                and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection

Claim 10; Page 79; 109pp; English.

mRNA from the known hybridoma F105 was converted to cDNA and this subjected to PCR amplification using primers corresp. to appropriate parts of the heavy or light chains and having restriction sites to permit cloning. The extension prods, were isolated and sequenced. The recombinant human monoclonal antibody (MAb) blinds to a discontinuous epitope on the HIV gpl20 envelope glycoprotein, blocks the binding of gpl20 to the CD4 receptor, and neutralises a broad range of HIV isolates. The MAb may be used to treat immune deficiency, can at Ances of 1.10 m.74.
                                                                                                                                                                                                                                                                                                                                        10-DEC-1991; US-804652.
10-DEC-1991; US-804652.
(DAND ) DANA FARBER CANCER INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL
                                                                                                                              deficiency,
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F105 rearranged variable i Monoclonal antibody; MAb; CD4; receptor; hybridoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immortalised by EBV transformation, and plated and assayed for activity. Clones which showed positive reactivity with autologous tumour cells from the patient and the SCLC cell line NCIH69, were subjected to limiting dilution to prepare the MAb. Sequence 134 AA:
                                                                                                                                                                                                                                                                                                                        N-PSDB; Q49155
                                                                                                                                                                                                                                                                                                        DNA segments encoding
                                                                                                                                                                                                                                                                                                                                     WPI; 93-214174/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                   W09312232-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1993 (first entry)
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10-DEC-1992; U10928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain;
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STRATGIPDRESGSGSGTDFILTISRLEPEDFAVYYCQQYGSSARYIFGQGTKLEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRATGIPARFSGSGSGTEFTLTISSLQSEDFAYYYCQQYNNWPPYTFGQGTKLEIKR 117
                                                          100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epitope; immune deficiency.
                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                              esp. at doses of 0.1-10 mg/kg. 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 AA;
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=_sig_peptide
20. .129
/label=_mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                       81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%;
                                                                                                                                                                                                                                                                                             monoclonal antibody -
for treating AIDS, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    le region light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           envelope; glycoprotein; gp120; HIV; polymerase chain reaction; PCR; heav
                                                                      Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 504.5; DB 1
Pred. No. 4.8e-31;
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                                                         Mismatches
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                                                                      499; DB 1;
No. 1.2e-30;
                                                                                                                                                                                                                                                                                                                                                CORP.
Sodroski JG;
                                                                                                                                                                                                                                                                                           which binds to for diagnosing
                                                         9:
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                                                                                   Length 129
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TTTTTTTESKKKETC
                                                                                       Query Match
Best Local Sir
Matches 100;
                                                                                                                                             and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection
Disclosure; Page 74-75; 109pp; English.
The nucleotide sequence of F105 Vk (Q42707 - sequence differs other F105 Vk sequences given elsewhere in the specification) compared with germiline gene Humvk325 (Q42706), showing 97.7% similarity. By nucleotide sequence analysis, F105 appears to be derived from a member of the Vk III subgroup gene family. Sequence 129 AA;
                                                                                                                                                                                                                                                                              24-JUN-1993.
10-DEC-1992; U10928.
10-DEC-1991; US-804652.
(DAND ) DANA FARBER CANCER INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL
(NEWE-) NEW A. MATASCO WA, POSDER MR,
                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "Leu
misc_difference 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_difference
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01-NOV-1993
                                                                                                                                                                                                                                                 DNA segments encoding
                                                                                                                                                                                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
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                                                                                                                                                                                                                                                               N-PSDB; Q42706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lomo sapiens
                      8
                                                                                                   Local Similarity
  73
                                           13
           STRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPYTFGQGTKLEIKR 117
                                                        LWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVS-SNLAWYQQKPGQAPRLLIYGA 59
                                                                                                                                                                                                                                                                         93-214174/26.
SSRATGIPDRFSGSGSGTDFTLTISRVEPEDFAVYYCQQYDN-SVCTFGQGTKLEIKR 129
                                          LWLPDTTGEIVLTQSPGTLSLSAGERATLSCRASQSVSRSYLAWYQQKPGQAPRLLIYGA 72
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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116
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                                                                                                                                                                                                                                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR2
l10. .117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label- F105Vk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= mat_protein
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                                                                                                80.8%;
                                                                                                                                                                                                                                      for treating AIDS, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .129
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                                                                                      Score 497; DB
Pred. No. 1.7e
7; Mismatches
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Sodroski JG;
                                                                                      DB 1; I
1.7e-30;
les 9;
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                                                                                                            Length 129;
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Best Local S
Matches 98
W09106305-A.
16-MAY-1991.
06-NOV-1990; U06425.
07-NOV-1989; US-432700.
(BRIM ) BRISTOL-MYERS SQ
Shuford WW, Harris LJ, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the human Hil monoclonal antibody variable (V) region heavy (H) chain which specifically recognises the C-antigen. Such an antigen binding fragment may be used for treating a patient with nepplasia. It is especially useful in the detection of lymphomas and leukaemias where the tumour cells bearing the C antigen are circulating in the patients bloodstream. The polynucleotide sequence may be used as primer or a probe and the encoded protein may be used in a vaccine or for gene therapy. The human monoclonal antibody (MAb), designated Hil, specifically recognises cancerous cells. Hil is specific for gine therapy. The human monoclonal antibody may be used in a vaccine or specifically recognises cancerous cells. Hil is specific for gine therapy. The human monoclonal antibody may be used in a vaccine or specifically recognises cancerous cells. Hil is specific for gine therapy. The human monoclonal antibody may be designated Hil, specifically recognises cancerous cells. Hil is specific for gine therapy. The human monoclonal antibody may be designated with the protein may also be used to the control of the protein may also be used to the control of the protein may also be used to the control of the protein may also be used to the control of the protein may also be used to the protein may be used to the protein may also be used to the pr
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Antigen binding fragment from monoclonal antibody, Hi tumour specific detection and treatment of neoplasia claim 1; Page 87-88; 126pp; English.

Claim 1; Page 87-88; 126pp; English.
                                                                                                                                                                                                                                                                      ORF 1 of IgG light chain variable region clone. immunoglobulin G; light chain; variable region; passive immunity; group B streptococci.
                                                                                                                                                                                                                                                                                                                                                      R12129 standard; Protein; 401
R12129;
01-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human monoclonal antibody H11 protein variable region H chain. H11; monoclonal antibody; MAb; C-antigen; variable region heavy V region; H chain; neoplasia; detection; lymphoma; tumour cell; primer; vaccine; gene therapy; glioblastoma; neuroblastoma; malignant melanoma; adenocarcinoma; small cell lung carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W40069 standard; Protein; 150
W40069;
29-MAY-1998 (first entry)
                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO-) NOVOPHARM BIOTECH IN Dan MD, Kaplan HA, Maiti PK; WPI; 98-018515/02.
                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to detect C-antigen in a sample.
Sequence 150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9744461-A2.
27-NOV-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRATGMPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPQTPQITFGGGTKVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNN----WPPYTFGQGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                       /note-
region"
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                                                                                                                                                           "last 3 amino acids of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 494; DB Pred. No. 3.2e 9; Mismatches
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3.
                                                                                                                                                                                                                                                                                                        region;
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.2e-30;
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                                                                                                                                                                leader and
                                                                                                                                                                                                                                                                                                        duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 150;
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Best Local
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                                                                                                                                          The MAb, or a fragment, can be used to inhibit the growth of tumour cells, especially late stage prostatic tumour cells in humans, optionally conjugated to a cytotoxic agent, especially doxorubicin, taxol or cisplatin, or a signal transduction, ras or cell annihibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Fig 17; 104pp; English.

This sequence is derived from funcheotide sequence encoding the light chain variable region. The "x" residues represent nonsense codons. The coding sequence has been translated in all 3 reading frames (see also R1213) and R12131). The L'V region is duplicated in so-called "aberrant" light chains (see Q11878), conferring increased avidity on antibodies comprising such aberrant chains.
                                                                                                                                                                                                                                                                                                                                       (IMCL-) IMCLONE SYSTEMS INC.
(MRCC-) MRC COLLABORATIVE CENT.
GLOTGIO NA, GOLDStein NI, Jon
MPI; 97-051897/05.
N-PSDB; T49345.
                                                                                                                                                                                                                              Claim 31; Fig 19; 112pp; English.
The present sequence is the kappa light chain variable region of the reshaped human monoclonal antibody (MAb) H225, 225RKA.
MAb is specific for the human epidermal growth factor (EGF)
                                                                                                                                                                                                                                                                                                           Chimeric and humanised versions used for inhibiting tumour grow
                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1996.
07-JUN-1996; U09847.
07-JUN-1995; US-482982.
15-DEC-1995; US-573289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
WO9640210-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1997 (first entry)
Kappa light chain variable region of 225RA antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wPI; 91-163947/22.

N-PSDB; Q11879
Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
Oligomerous immunoglobulin(s) with high avidity for antigen(s) -
formed by duplicating esp. variable region of light chain of igg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W08946 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221
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 13
                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTR 62
               LWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LWLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSIGTNIHWYQQRPGQAPRLLIKYAS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   light chain; reshaped; monoclonal; antibody; 225RA; epidermal growth factor; EGF; receptor; inhibition; grow cell; late stage; prostatic; prostate; variable region.
                                                        94; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 AA;
                                                          Conservative
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                                                                      79.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                         growth,
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                                                                                                                                                                                                                                                                                                                                                                     Jones
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Pred. No. 8.8e-30;
7; Mismatches 11;
                                                       Score 490.5; DB 1;
Pred. No. 5e-30;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹
                                                                                                                                                                                                                                                                                                                                                                    ST,
                                                                                                                                                                                                                                                                                                         anti-EGF receptor antibody 225 esp. of late stage prostatic
                                                                                                                                                                                                                                                                                                                                                                     Saldanha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 401;
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                                                                                    Length
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                                                     Gaps
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26-APR-1493; 22-JUL-1993; 18-NOV-1993;

US-053131. US-096762. US-155301. US-161739.

10-NOV-1994. 25-APR-1994; WO9425585-A.

004580

Transgenic mouse; transgenic animal; antibody engineering; variable region; light chain; minilocus transgene; chimeric antibody.

07-JUN-1995 (first entry) Human V-kappa vk65.3 region.

R62928

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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 21% Fig 41; 196pp; English.

The V-kappa specific oligonucleotide 050327 was used to probe a numan placental genomic DNA library cloned into lambdaEMBL3/SP6TT.

DNA fragments containing V-kappa segments from positive phage clones were subcloned into plasmid vectors. Variable gene segments from the resulting clones were sequenced and functional clones were selected on the basis of open reading frames, intact donor and acceptor splice sites and intact recombination sequences. The sequences obtained from four different plasmid clones were designated p55.3, p65.8, p65.8 and p65.15 (see Q44222-Q44225, respectively) and the amino acid sequences of the V-kappa regions considered were deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; 044222.
Transgenic non-human animals contg. immunoglobulin heavy chain
trans gene - used to produce useful antibodies by isotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human V-kappa fragment encoded by clone vk65.3.
Immunoglobulin; light chain variable region; minilocus;
isotype switching; unrearranged functional Vk gene segment;
                                                                                                                                                                                    R62928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENP-) GENPHARM INT INC Kay RM, Lonberg N; WPI; 93-214169/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R38648 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-NOV-1993
                                                                                                                                                                                                                                                                61 TRATGIPARESGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP
                                                                                                                                                                                                                                                                                                        <u>1</u>3
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US-810279.
US-853408.
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Pred. No. 5.8e-30;
5; Mismatches 5;
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10-DEC-1993; US-165699.
09-MAR-1994; US-209741.
(GENP-) GENPHARM INT INC.
KAY RM, LONDERG N;
WPI; 94-358263/44.
N-PSDB; Q78852.
                Transgenic non-human animals producing heterologous or chimeric antibodies for binding a pre-determined human antigen with increased affinity
Disclosure; Fig. 41; 296pp; English.
Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in 078852-078855, respectively) each contain a V-kappa gene segment that can be used to form a complete human light chain minilocus transgene for expression in a nonhuman transgenic animal for heterologous antibody production. The deduced amino acid seguences of the V-kappa coding regions are given in R62928-R62931.
  Sequence
115 AA;
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ş 밁 Š st Local Similarity 90.3%; St Local Similarity 90.3%; Matches 93; Conservative Score 489; DB 1; I Pred. No. 5.8e-30; 5; Mismatches 5; Length 115; Indels 0 Gaps

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Search completed: July 26, 2000, 14:01:27 Job time: 2766 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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3

### Title: Perfect score: Sequence: Result No. Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB Maximum DB Scoring table: Run OM protein -9 number of Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 527 526.5 525.5 525.5 523 518.5 511.5 511.5 511.5 510.5 510.5 510.5 510.5 510.5 510.5 588.5 574.5 562 539.5 530.5 Score seq protein search, using sw model length: 0 length: 1000000 hits satisfying chosen parameters: PIR\_64:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Query Match US-09-203-768A-4 615 1 LWLPDTTGEIVMTOS 178050 seqs, 61884766 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 July 26, 2000, 14:21:22; Search time 43.23 Seconds (without alignments) 167.488 Million cell updates/sec LWLPDTTGEIVMTQSPATLS.....QYNNWPPYTFGQGTKLEIKR 117 pir1:\* pir2:\* p1r4:\* pir3:\* DB K3HUHA K49532 S46369 S38643 S40345 K3H07HI S40371 K3H07M A32274 A32274 A32274 S20636 S20636 S20636 S20636 K3HUCL S34005 S46375 SUMMARIES Ig kappa chain v-J Ig kappa chain - h Ig kappa chain - h Ig kappa chain v r Ig kappa chain v-J Ig kappa chain v-I Description

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S20631 C30608	H30601 G44151	S41816 I30608	S20633 JE0243	K3HUVG S40325 S40327	K3HU41 S40346 S23628 S40344
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Ig kappa Ig kappa			Ig kappa Ig kappa		Ig kappa Ig kappa Ig kappa Ig kappa
chain - h chain V-I	chain V r chain V-I chain V r		chain - h chain NIG	chain pre chain - h chain - h	chain pre chain V-J chain V r chain V-J

# ALIGNMENTS

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A; Reference number: \$40312 MULD: 94080891 A; Accession: \$40362 A; Status: preliminary; translation not shown A; Molecule type: GRNA A; Residues: 1-117 KKLES A; Residues: 1-117 KKLES A; Residues: 1-117 KKLES C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Superfamily: immunoglobulin V region; immunoglobulin homology E; 26-100/Domain: immunoglobulin homology <imm></imm>	RESULT 2 \$40362 Ig kappa chain - human C;Species: Homo sapiens (man) C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: \$40362 R;Klein, R.; JeenTchen, R.; Zachau, H.G. Eur. J. Immunol. 23, 3248-3271, 1993 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.	QY 1 LWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS 60	Query Match 95.7%; Score 588.5; DB 2; Length 128; Best Local Similarity 97.4%; Pred. No. 3.8e-42; Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;	A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-128 <kle> A;Cross-references: EMBL:X72453; NID:g441374; PIDN:CAA51121.1; PID:g441375 A;Cross-references: EMBL:X72453; NID:g441374; PIDN:CAA51121.1; PID:g441375 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin</kle>	S40343 Ig kappa chain V-J region - human C;Species: Homo sapiens (man) C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: S40343 R;Klein, R.; Jaenichen, R.; Zachau, H.G. Eur. J. Immunol. 23, 3248-3271, 1993 A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891 A;Accession: S40343

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                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-123 < KL
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Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi
A;Reference number: S40312; MUID:94080891
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A;Title: Expressed human immunoglobulin chi genes
A;Reference number: $40312; MUID:94080891
A;Accession: $40328
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Best Local S
Matches 112
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;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #téxt_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS 60
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LMLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105;
                                                                                                                                                                                                                                  1-123 <KLE>
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                                                                            87.7%;
87.3%;
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                                                                                                                                                       homology
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Pred. No. 5.9e-40;
5; Mismatches 7
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Pred. No. 4.9e
1; Mismatches
                                                                          Score 539.5; DB
Pred. No. 4e-38;
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                 genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.9e-41;
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light ( hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobuli F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x;Jlrik, F.R.; Sorge, J.; Fong, S.; Heitzmann, J.G.; Curd, J.G.; Chen, P.P.; Goldfien Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
A;Title: Cloning and sequence determination of a human rheumatoid factor light-chain A;Reference number: A01898; MUID:86177570
A;Accession: A01898
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A; Residues: 1-128 <NIC>
A; Residues: 1-128 <NIC>
A; Cross references: GB:L41174; NID:g762823; PIDN:AAA64877.1; PI
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
E; 36-110/Domain: immunoglobulin homology <IMM>
F; 70-76/Region: framework z
F; 70-76/Region: complementarity-determining
                                                                                           F;21-115/Product: rheumatoid factor, Ig kappa
F;21-43/Region: framework 1
F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:IGKV3
A;Cross-references: GDB:1:
A;Map position: 2p12-2p11
A;Introns: 17/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 04-Dec:1986 *sequence_revision 04-Dec:1986 *text_change 21-Jan-2000
C;Accession: A01898
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A; Residues: 1-115 <JIR>
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A;Accession: A56701
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C:Accession: A56701
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                                                                    F;44-54/Region: complementarity-determining
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R; Nickerson, K.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 NRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW-PRSFGQGTKVEIKR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LWLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDAS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPP-YTFGQGTKLEIKR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               the sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A. 270, 12457-12465, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V region precursor (HuA) - o sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                    rheumatoid factor, Ig kappa chain V-III region (CLL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Was
                                                                                                                                                                                                                                                                                                                                                                                                                                                               determined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 530.5; DB 2
Pred. No. 2.3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CLL) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                               the germline
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complementarity-determining

F;43-108/Disulfide

bonds:

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                                                                                                             A; Note: the sequence was determined from the differentiated gene C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F; 36-110/Domain: immunoglobulin homology <IMP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-115 <LIU>
                                                                                                                                                                                                                                                Liu, M.F.; Robbins, D.L.; Crowley, J.J.; Sinh
Immunol. 142, 688-694, 1999
Title: Characterization of four homologous L
Reference number: A30553; MUID:89093959
RACCESSION: A30553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title: Nucleotidic sequence analysis of Reference number: S34001; MUID:93209281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1-107 <MAR>
                                                                                                                                                                                                                                   Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                 J kappa chain precursor V-III region (Hah) - human (fragment)
Species: Homo sapiens (man)
Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL: Z18330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 Accession: A30553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mariette, X.; Tsapis, A.; Brouet, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cappa chain V region - human
cles: Homo sapiens (man)
cle: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change
    y Match 85.5%;
Local Similarity 97.1%;
hes 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYRNW-PRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPYTFGQGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S34005; S30524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.7%; ilarity 97.1%; Conservative
                                                                                                        immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                           D.L.; Crowley, J.J.; Sinha, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.6%;
Score 526; DB 2; 1
Pred. No. 4.9e-37;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 526.5; DB 2
Pred. No. 4.2e-37;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 527; DB 1;
Pred. No. 4.1e-37;
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                                            Length 115;
                                                                                                                                                                                                                                                                                                                                       Kozin, F.; Kipps, T.J.; Carson,
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    Indels
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Matches

100;

Conservative

Query Match Best Local Similarity

85.0%; .91.7%;

Score 523; DB 2; Pred. No. 8.8e-37;

Length 116; indels

Gaps

0

Mismatches:

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J. Biol. Chem. 262, 3671-3673, 1987
A;Title: Atypical glycosylation of an IgG
A;Reference number: A92630; MUID:87137666
A;Accession: B26555
A;Molecnia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region A, Reference number: PLO106; MUID:89235583
A;Molecuia +----
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C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                               A; Molecule type: protein A; Residues: 1-116 <MID>
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                                                                                                                                                                                                                                                                           Ig kappa chain V-III region (Ger) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;109-115/Region: complementarity-determining F;116-127/Domain: J region <JRG> F;128-144/Domain: C region (fragment) <CRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-144 <SIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;36-110/Domain: V region <VRE>
                                                                                                                                                                                                                                 ;Species: Homo sapiens (man)
;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44-54/Region: complementarity-determining 170-76/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20/Domain: signal sequence #status
                                                                                                                                                                                                                                                                                                                                                                                       73
                                                                                                                                                                                                                                                                                                                                                                                                        61 TRATGIPARESGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPYTFGQGTKLEIKR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
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les 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 LWLPDTTGEIVMMQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGAS
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                                                                                                                                                                                                                                                                                                                                                                                    NRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW-PLTFGGGTKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQRPGQAPRLLIYDAS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heterotetramer; immunoglobulin
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Pred. No. 6.7e-37;
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                                           homology
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: $40326
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes
A;Reference number: $40312; MUID:94080891
A;Accession: $40326
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                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-128 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                  ;Cross-references: EMBL:X72489; NID:g441446; PIDN:CAA51157.1; PID:g441447; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Homo sapiens (man)
Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translation not shown
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Best Local Similarity
                                                                                                                                          Matches 100;
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Best Local Similarity
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uperfamily: immunoglobulin V region; immunoglobulin
eywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                             le: Expressed human immunoglobulin chi genes prence number: S40312; MUID:94080891 cession: S40379
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73
               61 TRATGIPARFSGSGSGTEFTLTISSLQSEDFAYYYCQQYNNWPPYTFGQGTKLEIKR 117
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                                                                                             LWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS 60
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RESULT JE0244

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C;Species: Homo, sapiens (man)
C;Species: Homo, sapiens (man)
C;Date: (05-Dec-1998 #sequence_revision 05-Dec-1
C;Accession: JE0244
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, submitted to JIPID, November 1998
submitted to JIPID, November 1998
                                                              Ig kappa chain V-J region (T33-5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan 1995 *sequence_revision 01-Sep-1995 *
                                                                                                                                           RESULT
S46375
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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                      C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000 C;Accession: S46375; S38648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z17330; NID:g38511; PIDN:CAA78978.1; PID:g38512
A;Note: human sequences cloned and sequenced prior to expression in mouse myeloma
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Walls, M.A.; Hs1ao, K.; Harris, L.J.
Nucleic Acids Res. 2, 2921-2929, 1934
A;Title: Vectors for the expression of PCR-amplified immunoglobulin
A;Reference number: S34110; MUID:93324379
A;Accession: S34110
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A; Reference number: JE0244
A; Mccession: JE0244
A; Mccledie type: protein
A; Residués: 1-215 <ALI>C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPYTFGQGTKLEIKR 117
C.; Chastagner, P.;
2951-2962, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -129 <WA2>
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                        Zouali, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 513.5; DB 2;
Pred. No. 5.9e-36;
Pred. No. 5.9e-36;
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Pred. No. 8.8e-36;
5; Mismatches 6
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Search completed: July 26, 2000, 14:21:23 Job time: 3443 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein protein search, using sw model

Run on:

July 26, 2000, 14:25:25; Search time 12.18 Seconds (without alignments) 297.679 Million cell updates/sec

Title: Perfect score: US-09-203-768A-4 615 1 LWLPDTTGEIVMTQ:

Sequence: LWLPDTTGEIVMTQSPATLS.....QYNNWPPYTFGQGTKLEIKR 117

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

85661 segs, 30989116 residues

number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_38:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Score Match Length DB ID    Score Match Length DB ID   Description	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Result No.
Ouery Match Length DB         ID         Description           96.1         129         1         KV3H_HUMAN         P04207 homo           96.1         129         1         KV3L_HUMAN         P18135 homo           82.9         129         1         KV3L_HUMAN         P18135 homo           82.0         109         1         KV3L_HUMAN         P04231 homo           90.2         128         1         KV3L_HUMAN         P04433 homo           74.6         116         1         KV3L_HUMAN         P01620 homo           73.8         109         1         KV3L_HUMAN         P01623 homo           71.5         108         1         KV3L_HUMAN         P01623 homo           71.5         108         1         KV3L_HUMAN         P01623 homo           71.5         108         1         KV4L_HUMAN         P01619 homo           70.8         109         1         KV3L_HUMAN         P01619 homo           71.5         108         1         KV4L_HUMAN         P01619 homo           70.1         1         KV4L_HUMAN         P01621 homo           70.6         114         1         KV4L_HUMAN         P01621 homo           61.5<	33 38 39 55 55 55 55 55 55 55 55 55 55 55 55 55	Score
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Query Match 96.1 Best Local Similarity 94.9 Matches 111; Conservative

96.1%; Score 591; DB 1; Length 129; 94.9%; Pred. No. 6.3e-51; tive 4; Mismatches 2; Indels

Gaps

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45	44	43	42	41	40	39	38	37	36	35	34
366.5	367.5	367.5	368	368.5	369.5	370.5	370.5	370.5	371	377.5	378.5
59.6	59.8	59.8	59.8	59.9	60.1	60.2	60.2	60.2	60.3	61.4	61.5
111	111	108	133	111	111	136	111	108	112	108	108
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P18136;
01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P18135;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
15-UL-1999 (Rel. 18, Last annotation update)
16 KAPPA CHAIN V-III REGION HIC PRECURSOR.
Homo sapiens (Human)
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DISULFID
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"Autoantibody-associated kappa light chain variable region
expressed in chronic lymphocytic leukemia with little or no
mutation. Implications for etiology and immunotherapy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation. Implications for etj
J. Exp. Med. 167:840-852(1988)
-1- DISEASE: THE PROTEIN IS ON
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                  SEQUENCE FROM N.A. MEDLINE; 88171307. Kipps T.J., Tomhave
                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin
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HSSP; P01789; 2MCP.
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    Autoantibody-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LWLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYGA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTOANTIBODIES EXPRESSED
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                                                                                                                                                                                                                                                                                                                                                                                                    SSRATGIPDRESGSGSGTDFTLTISRLEPEDFAVYYCQQYGT-SPRTFGQGTKVEIKR 129
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oglobulin V r
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Primates;
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                         Chen P.P.,
  kappa light
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D IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 510; DB 1;
Pred. No. 4.7e-43;
7; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK 3
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                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                            tation update)
PRECURSOR.
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                      Carson D.A.
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on update)
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                                                                             HSSP; PO1789; AND.
HSSP; PO1789; AND.
PFAM; PF00047; 19; 1.
Immunoglobulin V region.
23 89
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P01624;
21-JUL-1986 (Rel. 0
21-JUL-1986 (Rel. 0
21-JUL-1999 (Rel. 3
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PIR; PL0021; K3HUHI.

HSSP; P01789; 2MCP.

PFAM; PF00047; 1g; 1.

Immunoglobulin V region; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed in chronic lymphocytic leukemia with little mutation. Implications for etiology and immunotherapy J. Exp. Med. 167:840-852(1988).

-I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOCAUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC
                                                           SEQUENCE
                                                                                                                                                      Ann.
                                                                                                                                                                             from
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                      NON_TER
                                                                                                                                                                                                                                                                     fomo sapiens (Human)
                                                                                                                                                                                                                                                                               11-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION POM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                        SEQUENCE.
                                                                                                                                                                                                               EDLINE; 76276460
Local Similarity 90.9 los 100; Conservative
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                                                                                                                                          GLOBULIN ACTIVITY.
                                                                                                                                                      MISCELLANEOUS: THIS CHAIN WAS
                                                                                                                                                                                     per D.G., Capra J.D.;
amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             SSRATGIPDRESGSGSGTDFTLTISRLEPXDFAVYYCQQYGS-SPWTFGQGTKVEIKR
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                                                                                                                                                                          two idiotypically cross
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109 AA;
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                                                                                                                                                                        sequence of the variable regions of the light chains pically cross reactive IgM anti-gamma globulins.";
                                                          11922 MW;
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118
            82.0%;
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 Score 504; DE
Pred. No. 1.5e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
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O IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                             BY SIMILARITY.
                                                                                                                                                               reactive IgM anti-gamma 127C:261-271(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 5.9e-43;
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
JK1 SEGMENT.
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COMPLEMENTARITY-DETERMINING 1.
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                                                          62821DDC6A8ABA86 CRC64;
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            DB 1;
.5e-42;
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                               KV3I_HUMAN
P04433;
13-AUG-1987
13-AUG-1987
15-JUL-1999
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DOMAIN
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13-AUG-1987 (Rel. 05, L
15-UUL-1999 (Rel. 05, L
15-UUL-1999 (Rel. 38, La
'G KAPPA CHAIN V-III REG
'2mo sapiens (Huma-'
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Klobeck H.G., Meindl A.,
                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z00021; CAA77316.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human immunoglobulin
III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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1-JAN-1988
5-JUL-1999
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-JUL-1999 (Rel. 38, Last annotation update)
KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                       A01899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRANGIPDRESGSGSGTDETLIISRLEPEDEAVYYCQQYST-SPYTEGQGTKLEIKR
                                                                                                                                                      TRATGIPARESGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPYTFGQGTKLEIKR 117
                                                                                                                                                                            LWLPDTTGEIVLTQSPGTLSLSPGESATLSCRASQSVSSNLAWYQQKRGQSPRLLIRDAS 72
                                                                                                                                                                                                LWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS 60
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97; Conser
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1108
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                     , Last sequence update)
, Last annotation update)
REGION VG PRECURSOR (FRA
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                                                                                                                                                                                                                      Score 493.5; DB 1;
Pred. No. 1.9e-41;
7; Mismatches 12;
                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY-DETERMINING JK1 SEGMENT. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                         IG KAPPA CHAIN V-III REGION FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                     FRAMEWORK
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                       PRECURSOR (FRAGMENT).
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subgroups II
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PFAM; PF00047; 19; J
Nucleic Acids Res. 12(2)29236(1984).

This SWISS-PROT entering produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SEQUENCE
                                                                                                                                                                                                              SEQUENCE;
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P04434;
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DOMAIN
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                                                                                                                                                        Pech M., Zachau H.G.;
"Immunoglobulin genes
within the VK locus.";
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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Mammalia; |
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                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III REGION VH PRECURSOR (FRAGMENT).
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Immunoglobulin genes
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85087932.
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Eutheria;
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COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
BY SIMILARITY.
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Pred. No. 4.5e-41;
5; Mismatches 5
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                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Hqmo.
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MEDLINE; 82046598.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PFAM; PF00047; 1g; 1.
Immunoqlobulin V region;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG KAPPA CHAIN V-III REGION SIE.
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Amino acid sequence of the variable regions of light chains from two
idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
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; P01789; 2MCP.
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ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPYTFGQGTKLEIKR 117
                                                                              EIVMTQSPATLSVSPGERATLSCRASQSVS-SNLAWYQQKPGQAPRLLIYGASTRATGIP 67
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Pred. No. 1.1e-37;
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COMPLEMENTARITY-DETERMINING
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KV3E_HUMAN
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KV3D_HUMAN
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HSSP; P01789; 2MCP.
PFAM; PF00047; 1g; 1.
Immunoglobulin V region; B
PIR; A01896; K3HUWL.
HSSP; P01789; 2MCP.
FFAM; PF00047; 1g; 1.
Immunoglobulin V region.
DISULFID 23 89
                                                                                                                                                                                                                                 KV3E_HUMAN STAN
P01623;
P01623;
21-JUL-1986 (Rel. C
21-JUL-1998 (Rel. C
15-JUL-1999 (Rel. C
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NON_TER
SEQUENCE
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Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

"Rule of antibody structure. The primary structure o
immunoglobulin L-chain of kappa-type, subgroup 3 (Be
                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                    Blochemistry 20:5816-5822(1981)
                                                                                                group
                                                                                                         Andrews D.W., Capra J.D.; "Amino acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the mechanism of antibody production.";
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
-i- MISCELLANEOUS: THE C. REGION OF THIS CHAIN HAS T-
-i- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; J
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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21-JUL-1986
                                                                                                                                                                                                                                                                                                                                           61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS-SPSTFGQGTKVELKR
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                                                            GLOBULIN ACTIVITY.
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109 AA;
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11788 MW;
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81.8%;
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BY SIMILARITY.
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                                                                                                                                                                                    Hominidae;
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Best Local Similarity 77.1
Matches 84; Conservative
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   MEDLINE; 77038198.
Capra J.D., Klapper D.G.; "Complete amino acid sequ
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Homo sapiens (Human).
Homo sap
                                                                                                                                                                                                                                                               KVIM_HUMAN STANDARD; PRT; 108 AA. P01605; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) IG KAPPA CHAIN V-I REGION LAY.
                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
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ISSP; P01789; 2MCP.
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Immunoglobulin V region;
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11746 MW;
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82.7%;
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BY SIMILARITY.
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Pred. No. 2.4e-36;
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                                                                                                                                                                        Catarrhini; Hominidae;
                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
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.le-37;
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HSSP; P01607; 1REI.
PFAM; PF00047; 1g; 1.
Immunoglobulin V region.
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                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a cubetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and following entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-APR-1988 (Rel. 07, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG KAPPA CHAIN V-IV REGION B17 PRECURS
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _HUMAN
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01-JAN-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
specificities.";
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Marsh P., Mills F.
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HSSP; P01789; 2MCP.
PFAM; PF00047; 1g; 1.
Immunoglobulin V region;
                                                                                             EMBL; X02990; CAA26733.1;
PIR; A01905; K4HU17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISION TO 76.
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MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMM!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLOBULIN, ACTIVITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OCT-1986) to the EMBL/GenBank/DDBJ databases
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Pred. No. 6.7e-36;
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING
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Amino acid sequence of a light chain variable region of a
prheumatoid factor of the Maidotypic group, in part predic
reactivity with antipeptide antibodies.";
Mol. Immunol. 23:239-244(1986).
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PFAM; PF00047; 19; 1.
Immunoglobulin V region.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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20-MAR-1987
15-JUL-1999
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PIR; A01893; K3HUGO.
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-MAR-1987 (Rel. 04, Last sequence update)
-JUL-1999 (Rel. 38, Last nnotation update)
KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
           ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPYTFGQGTKLEIKR
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                                         EIVLTQSPGTLSLSPGERATLSCRAALLSSRGYLAWYQQKPGQAPRLLMYGASSRATGIP
                                                       EIVMTQSPATLSVSPGERATLSCRAS-QSVSSNLAWYQQKPGQAPRLLIYGASTRATGIP
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DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS-SPRSFGQGTKVEIKR
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78.2%;
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                                                                                                  Score 428; DB 1;
Pred. No. 3.6e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 429.5; DB 1;
Pred. No. 3.3e-35;
6; Mismatches 14;
                                                                                                                                                                     BY SIMILARITY
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KV4B_HUMAN
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PFAM; PF00047; ig;
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PIR; A01904; K4HUJI.
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updating KAPPA CHAIN V-IV REGION JI PRECURSOR.
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Mammalia; Eutheria;
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                                                       55 LIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPDYTFGQGTKLE 114
                                                                                          13
                                             73 LIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYDTIP--TFGGGTKVE
                                                                                                     1 LWLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSV--SSN----LAWYQQKPGQAPRL 54
                      IKR 117
                                                                                      LWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKL
IKR 133
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FRAMEWORK 3.
COMPLEMENTARITY DETERMINING
FRAMEWORK 4.
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RESULT

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Best Local Similarity
Matches 41; Conserv
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SHIRASAWA T., OHNISHI K., HAGIWARA S., SHIGEMOTO K., TAKEBE Y.,

RAJEWSKY K., TAKEMORI T.;

"A novel gene product associated with mu chains in immature B cells.";

EMBO J. 12:1827-1834(1993).

EMBL; D13308; BAA02495.1; -.

MGD; MGI:98938; Vpreb3.

PFAM; PF00047; 19; 1.

CHAIN

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123

8HS20 PROTEIN.

SEQUENCE 123 AA; 13400 MW; DAZA70D3 CRC73:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPREB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8HS20 PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                    65 GIPARESGS--GSGTEFTLTISSLQSEDFAVYYCQQYNNWPP 104
                                                                                                                                                                                                                                                                                                                                                                                   12 MTQSPATISVSPGERATISCRA-SQSVSS---NLAWYQQKPGQAPRLIYGAST---RAT 64
                                                                                                                                                               82 DIPDRESATVDAAHNACILTISPVLPEDDADYFCSIAHTEEP 123
                                                                                                                                                                                                                                                                                                                           23 LTQ-PDAFSVFPGQDAHLSCTINSQHATAGDIGVSWYQQQPGSAPHLLYYYAEEEHYRPA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 145; DB 11;
Pred. No. 6.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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 Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9XSM6;
Q9XSM6;
01-NOV-1999
01-NOV-1999
01-NOV-1999
CD8 ALPHA CH
                                                                                                                                                                                                                                               Ol-JAN-1999 (ALTERNATION OF THE PRECURSOR.
CD8 BETA ANTIGEN PRECURSOR.
Felis slivestris catus (Cat).
Felis slivestris catus (Cat).
Felis slivestris (Cat).
Felis slivestris (Cat).
Felis slivestris (Cat).
Felis slivestris (Cat).
                                                              CHAIN
                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                     SEQUENCE
                                                                                             EMBL; AB000484; BAA19125.1; PFAM; PF00047; 1g; 1.
                                                                                                                                      MEDLINE; 97067796.
PECORARO M.R., SHIMOJIMA M.,
KAI C., MIKAMI T.;
                                                                                                                                                                                                    Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ130818; CAB41462.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular characterization of cDNAs esciureus) CD8 alpha and beta chains.";
Immunogenetics 49:718-721(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saimiri sciureus (Common squirrel monkey)
Eukaryota; Metazoa; Chordata; Craniata; V
                                                                                                                                                                                                               TISSUE=THYMUS;
MIYAZAWA T.;
                                                                                                                                                                                                                                                                                                                                           P79336
                                                                                                                 Molecular cloning of the feline CD8 [mmunology 89:84-88(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-92039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                      'ISSUE-THYMUS
                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRETA-VIDAL A., GARCIA Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDLINE;
                                                                                                                                                                                                                                                                                                                                                                                               13
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NOV-1999 (TrEMBLrel. 12
ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                               w
                                                                                                                                                                                                                                                                                                                                                                                              ADGLDAQRFSGKKMGDSFILTLRDFREEDQGFYFCSALSN 120
                                                                                                                                                                                                                                                                                                                                                                                                           ATGIPA-RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNN 101
                                                                                                                                                                                                                                                                                                                                                                                                                                      PSRFRVSPLDRTWNLGDKVELKCEVLLSNPSSGCSWLFQKRGAAASPTFLLYISQTKPKV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATLSVSP----
  l Similarity
32; Conser
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235 AA;
 Conservative
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210
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235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Ve
Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25728 MW;
            19.68;
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                                                                                                                                                                                                    the
                                                     WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEMONNIER F.A.,
Score 120.5; DB; Pred. No. 4e-05; Pred. No. 4e-05; Mismatches
                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 123; DB
Pred. No. 2.5e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                  POTENTIAL.
POTENTIAL.
; 915E2BD1
                                                                                                                                                MAEDA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CD8 ALPHA CHAIN.
; F22E0AB5 CRC32;
                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding squirrel monkey (Saimiri
                                                                                                                             beta-chain
                                                                                                                                                                                                                                                                                                                                          210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
                                                                                                                                                INOSHIMA Y.,
                                                     CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAZANJI M.;
                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 235
                      Length
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                 KAWAGUCHI Y.,
                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
                    210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
  25;
 Gaps
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RESULT

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Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                                              Q9Y4V0 PRELIMINARY;
Q9Y4V0;
01-NOV-1999 (TrEMBLrel. 1:
01-NOV-1999 (TrEMBLrel. 1:
01-NOV-1999 (TrEMBLrel. 1:
01-NOV-1999 (TrEMBLrel. 1:
01-NOV-1999 (SIRP-BETAI (S:
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Q9Y509;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAO J., VESCIO R.A., RETTIG M.B., HONG C.H. LICHTESTEIN A.K., BERENSON J.R.;
"A CD10-positive subset of malignant cells myeloma using PCR with patient-specific imm Leukemia 9:1948-1953(1995).
EMBL; S80860; AAD1439.1; -.
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases EMBL; AL049634; CAB46661.1; -. SEQUENCE 397 AA; 43037 MW; C9D81FC5 CRC32;
                                                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Entheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                       Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                           DJ576H24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                   MATTHEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 96071149.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 VQPGKSLRLSCEASGFTFSTYGMSWVRQAPGKGLDWVALISYDGSTQYYAGSVKGRFTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 VSPGERATLSCRASQSVSS--NLAWYQQKPGQA---PRLLIYGASTR--ATGIPARESGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 AA;
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                                                                                                                                                                                                                   Chordata; Cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.5%;
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                                                                                                                                                                                                                                                                                                                                                         . 12, Last sequence update)
. 12, Last annotation update)
(SIGNAL REGULATORY PROTEIN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2,72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Pred. No. 3e-05;
                                                                                                                                                                                                                                                     Craniata; Vertebrata;
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                                                                                                                                                                                                                       Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115
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Query Match Best Local Similarity

19.1%;

Score 117.5; DB 4 Pred. No. 0.00017;

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P78324; 000683;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR
(SHP SUBSTRATE-1) (INHIBITORY RECEPTOR SHPS-1) (SHPS-1) (SIGNAL-
REGULATORY PROTEIN ALPHA-1) (SIRP-ALPHA1) (MYD-1 ANTIGEN).
PTPNS1 OR SHPS-1 OR DJ684024.1.
                                                                          Signal; Transm
Glycoprotein;
SIGNAL
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PFAM;
                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ULLRICH A.;
"A family of proteins that receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-PLACENTA;
MEDLINE; 97215901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUJIOKA Y., KASUGA M.;
"Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal localization of genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
       DOMAIN
                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                     ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 146-503 FROM N.A. BATES K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 386:181-186(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 97223399.
YAMAO T., MATOZAKI T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KHARITONENKOV A., CHEN Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
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                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH
HIGH LEVELS ALSO PRESENT IN HEART, SPLEEN, TES
PERIPHERAL BLOOD LEUKOCYTES.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPE
TWO C1-LIKE AND ONE V-LIKE DOMAINS.
LI; D86043; BAA12974.1; -.
LI; Y10375; CAA71403.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEIK 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELQVIQPEKSVSVAAGESATLRCAMTSLIPVGPIMWFRGAGAGRELIYNQKEGHFPRVTT
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                                                                                                                                                                                      AL034562; CAB38874.1;
                                                                                                                                           PF00047; 1g; 3.
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                                                                                                                 Transmembrane; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biophys.
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       27
                                                                                             SH3-binding;
                                                  503
       372
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                                                                     POTENTIAL.
  PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE SUBSTRATE 1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                            IMMUNOGLOBULIN SUPERFAMILY. CONTAINS DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATSUDA Y., TAKAHASHI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signalling
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                                                                                                              Immunoglobulin domain;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-AUG-1999 (TrEMBLrel. 11, Last annotation update)
SIGNAL-REGULATORY PROTEIN BETA-1 PRECURSOR (SIRP-BETA1).
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Fiskarvota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KHARITONENKOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
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                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE I MEMBR SIMILARITY: BELONGS TO THE IMMUNOG TWO C1-LIKE AND ONE V-LIKE DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
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                                                                                                                                                                                                                                                                      domain; Glycoprotein;
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SH3-BINDING (POTENTIAL).
SH2-BINDING (POTENTIAL).
SH2-BINDING (POTENTIAL).
SH2-BINDING (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
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IG-LIKE C1-TYPE DOMAIN.
IG-LIKE C1-TYPE DOMAIN.
SH2-BINDING (POTENTIAL).
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IG-LIKE V-TYPE DOMAIN.
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IG-LIKE C1-TYPE DOMAIN.
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01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
01-MAY-1999 (TREMBLRE) 110, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION
Mus musculus (Mouse).
Eukharyota, Metazoa; Chordata; Craniata; Vertebrata; Ma
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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 SEQUENCE FROM N.A STRAIN-BALB/C;
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"Molecular characterization of cDNAs e
sciureus) CDB alpha and beta chains.",
Immunogenetics 49:718-721(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saimiri sciureus (Common squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; S
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32; Conserv
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Pred. No. 0.00028;
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Pred. No. 0.
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CD8 BETA CHAIN.
FCE8E996 CRC32;
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encoding squirrel
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01-MAY-1999 (
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SEQUENCE
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"Somatic hypermutation of the new antigen receptor gene (NAR) in nurse shark does not generate the repertoire: possible role in antigen-driven reactions in the absence of germinal centers.";

proc. Natl. Acad. Sci. U.S.A. 95:14343-14348(1998).
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"Humanized porcine vCAM-specific monoclonal antibodies IgG2/64 constant regions block human leukocyte binding endothelial cells.";

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases EMBL; U78801; AAD00293.1;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 99045686. DIAZ M., GREENBERG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
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136 AA;
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ilarity 30.6%;
Conservative 1
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Pred. No. 0.00042;
5; Mismatches 47;
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Matches 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Eutheria; Cetartiodactyla; Ru
                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Y298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TREMBLIE).
01-NOV-1998 (TREMBLIE).
01-NOV-1999 (TREMBLIE).
SURROGATE LIGHT CHAIN (I
                                                                                                                                                                                                                                                                                                                                                                                Blood 92:496-506(1998).
EMBL; AJZ24083; CAA11829.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9Y298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-BONE MARROW;
RAYCHEL A.P., HALLIGAN B.D.;
Submitted (MAY-1998) to the !
EMBL; AF068848; AAC19380.1;
HSSP; P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ224083;
Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPREB
                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ry Match
                                                                                                                                                                                                                                                                                                                                                                                                                         ACQUEMIN M.G., VANDER ELST L.P.L.;
"Mechanism and kinetics of factor VIII inactivation: study with an igg4 monoclonal antibody derived from a hemophilia A patient with inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A. EDLINE; 98322155.
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    74
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                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HKVPPRFSGSKDLAKNTGYLSIAELQA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- IPARFSGSGSGTEFT--LTISSLQS
  SGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVPDPDAFDIW
                                            TG--IPAR-FSGSGSGTEFTLT-----ISSLQSEDFAVYYC-----QYNNWPPYTFGQ 109
                                                                                        THAOVQLVQSGAEVK-KPGASVKVSCKVSGYTLTELPVHWVGQAPGKG--LEWVGSFDPE 73
                                                                                                                                 TTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLA--WYQQKPGQAPRLLIYGASTRA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLSQPPSVASFL-GATVRLACTLSSDHDVNLHSIYWYQQRPGHRPRFLLRYFSPSDKRQG
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100 AA;
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150 /
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(TremBLrel. 12, Last sequence update)
(TremBLrel. 12, Last annotation update)
SIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                Conservative
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A
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16031 MW;
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11142 MW;
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                                                                                                                                                                                             17.4%;
32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.6%;
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1. 08, Created)
1. 12, Last annotation update)
(FRAGMENT).
                                                                                                                                                                             18;
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                                                                                                                                                                           Score 107; DB
Pred. No. 0.00
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 108;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3785537C CRC32;
                                                                                                                                                                                                                                                                                          B18EC39A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                             43;
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                                                                                                                                                                                                                       Length 150
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စ်
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Best Local Similarity
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SEQUENCE :.....
STRAIN-WISTAR: TISSUE-BRAIN,
STRAINE: 98207252.

MEDLINE: 98207252.

NAKAZATO S., NOMOTO K., KAZAHARI K., ONO M.;
Physical linkage of the B29/Ig-beta (CD79B) gene to the skeletal muscle, sodium-channel, and growth hormone genes in rat and human Genomics 48:563-368(1998).

Genomics 48:563-368(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O46631 PRELIMINARY;
O46631;
O1-JUN-1998 (TrembLrel. (
O1-JUN-1998 (TrembLrel. (
O1-MAY-1999 (TrembLrel. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            070153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUR. J. Immunol. 28:1-11(1998).
EMBL; Y11046; CAA71943.1; -.
PFAM; PF00047; 19; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BROOKE G.P., PARSONS K.R., HOWARD C.J.;
"Cloning of two members of the SIRP alpha family of protein tyrosine phosphatase binding proteins in cattle that are expressed on monocytes and a subpopulation of dendritic cells and which mediate binding to CD4 T cells.";
                                                                                                                                                                                                                                                         Paritus norregicus (Rat).
Rattus norregicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TremBLrel.
01-AUG-1998 (TremBLrel.
01-MAY-1999 (TremBLrel.
B29/IG-BETA/CD79B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYD-1 ANTIGEN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                              B29/IG-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-PERIPHERAL BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP----PYTFGQGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEIVMTQSPATLSVSPGERATLSCR-ASQSVSSNLAW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
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506 MW;
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25.8%;
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Last sequence update)
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Last sequence update)
Last annotation updat
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MYD-1 ANTIGEN.
; 3D320629 CRC32;
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                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                              Rattus
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                                                                                                                  human.";
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                                                                                                                                                                                                                                                          Query Match 16.9%; Score 104; DB 4; Length 198; Best Local Similarity 32.0%; Pred. No. 0.0019; hes 32; Conservative 13; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 17.1%; Score 105; DB 11; Best Local Similarity 33.8%; Pred. No. 0.0018; Matches 27; Conservative 14; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3EQUENCE FROM N.A.

MEDLINE; 89215302.

MORMENT A.M., LONBERG N., LACY E., LITTMAN D.R.;

"Alternatively spliced mRNA encodes a secreted form of "Alternatively spliced mRNA of the human CD8 alpha gene.";

alpha. Characterization of the human CD8 alpha gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13970 PRELIMINARY; PRT; 198 AA.

013970;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00047; ig; 1. SEQUENCE 228 AA; 25865 MW; 03F8D7C6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                      J. Immunol. 142:3312-3319
EMBL; M26315; AAA79218.1;
EMBL; M26313; AAA79218.1;
EMBL; M26314; AAA79218.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 CQQKCNSTEPDVTDGCGTEL 139
                                                                                                                                                                                                                16 PATLSVSP-----GERATLSCRASQS-VSSNLAWYQQKPGQA--PRLLIYGASTR--- 62
                                                                                                    81
                                                                                                                             63 ATGIPA-RESGSGSTEFTLTISSLQSEDFAVYYCQQYNN 101
                                                                                                                                                                               21 PSQFRVSPLDRTWNLGETVELKCQVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 CQQYNN--WPPYTFGQGTKL 113
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                                                                                                 AEGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSN 120
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198 AA;
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AAA79218.1; JOINED.
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21585 MW; B8399CB1 CRC32;
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